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(54) Title: PARG, A GTPase ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1		
(57) Abstract The invention describes nucleic acids encoding the PARG protein, including fragments and biologically functional variants thereof. Also included are polypeptides and fragments thereof encoded by such nucleic acids, and antibodies relating thereto. Methods and products for using such nucleic acids and polypeptides also are provided.		

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PARG, A GTPase ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1**Field of the Invention**

This invention relates to nucleic acids and encoded polypeptides which interact with the
5 PTPL1 phosphatase and which are GTPase activating proteins. The invention also relates to
agents which bind the nucleic acids or polypeptides. The invention further relates to methods of
using such nucleic acids and polypeptides in the treatment and/or diagnosis of disease.

Background of the Invention

10 The Rho family of Ras-like GTPases, which includes Rho, Rac and Cdc42, control actin-
based cytoskeletal rearrangements (reviewed in Hall, *Annu. Rev. Cell Biol.* 10:31-54, 1994;
Zigmond, *Curr. Opin. Cell Biol.* 8:66-73, 1996). Rho regulates receptor-mediated assembly of
focal adhesions and stress fibers (Ridley and Hall, *Cell* 70:389-399, 1992), while Rac regulates
the formation of membrane ruffles (Ridley *et al.*, *Cell* 70:401-410, 1992) and Cdc42 controls the
15 formation of filopodia (Nobes and Hall, *Cell* 81:53-62, 1995). Rho proteins have also been
shown to be important in the regulation of cell proliferation (reviewed in Symons, *Trends*
Biochem. Sci. 21:178-181, 1996). As members of the Ras superfamily, Rho proteins function as
molecular switches, having an active, GTP-bound form, and an inactive, GDP-bound form. The
active, GTP-bound form, is negatively regulated by GTPase activating proteins (GAPs) which
20 enhance the intrinsic GTPase activity of Rho proteins. A number of GAPs that are active on
proteins of the Rho family have been identified (reviewed in Lamarche and Hall, *TIG* 10:436-
440, 1994). These include p50RhoGAP (Lancaster *et al.*, *J. Biol. Chem.* 269:1137-1142, 1994),
Myr5 (Reinhard *et al.*, *EMBO J.* 14:697-704, 1995), and p190 (Settleman *et al.*, *Nature* 359:153-
154, 1992) which are also active on Rac and Cdc42. Another GAP, p122-RhoGAP (Homma and
25 Emori, *EMBO J.* 14:286-291, 1995) appears to be specific for Rho.

Intracellular protein tyrosine phosphatases (PTPs) are a diverse group of proteins
involved in signal transduction (reviewed in Streuli, *Curr. Opin. Cell Biol.* 8:182-188, 1996).
They contain a conserved PTP domain which specifically dephosphorylates tyrosine residues
and, in addition, domains that regulate their subcellular localization and activity (reviewed in
30 Mauro and Dixon, *Trends Biochem. Sci.* 19:151-155, 1994). For example, the SH2 domains of
SHP-1 and SHP-2 enables these PTPs to localize to and interact with activated growth factor
receptors (Mauro and Dixon, 1994). Correct localization of PTPs is of importance, since the

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PTP domains usually have broad substrate specificity.

PTPL1 (Saras *et al.*, *J. Biol. Chem.* 269:24082-24089, 1994) also called PTP-BAS (Maekawa *et al.*, *FEBS Lett.* 337:200-206, 1994), hPTP1E (Banville *et al.*, *J. Biol. Chem.* 269:22320-22327, 1994) and FAP-1 (Sato *et al.*, *Science* 268:411-415, 1995), is a 250 kDa protein expressed in many tissues and cell lines. PTPL1 is fully described in PCT published application WO95/06735. It contains an N-terminal leucine zipper motif followed by a domain with homology to the Band 4.1 superfamily. Band 4.1-like domains are found in proteins involved in the linkage of actin filaments to the plasma membrane (Arpin *et al.*, *Curr. Opin. Cell Biol.* 6:136-141, 1994). Five PDZ domains [PDZ is derived from PSD-95 (Cho *et al.*, *Neuron* 9:929-942, 1992), Dlg-A (Woods and Bryant, *Cell* 66:451-464, 1991) and ZO-1 (Itoh *et al.*, *J. Cell. Biol.* 121:491-502, 1993), each of which contains three such domains] are present between the Band 4.1-like domain and the C-terminal PTP domain. These domain structures of about 90 amino acid residues have also been called GLGF repeats or DHRs and are identified in a variety of proteins (Ponting and Phillips, *Trends Biochem. Sci.* 20:102-103, 1995). A PDZ domain of PTPL1 has been shown to interact with the C-terminal tail of the membrane receptor Fas (Sato *et al.*, 1995) and PDZ domains of PSD-95 bind to the C-terminals of the NMDA-receptor and Shaker-type K⁺ channels (Kim *et al.*, *Nature* 378:85-88, 1995; Kornau *et al.*, *Science* 269:1737-1740, 1995). The crystal structures of two PDZ domains have recently been published (Doyle *et al.*, *Cell* 85:1067-1076, 1996; Morais Cabral *et al.*, *Nature* 382:649-652, 1996).

There exists a need to influence the receptor-mediated intracellular signal transduction pathways to treat disease. There also exists a need to identify the gene(s) responsible for increased or decreased signal transduction and to provide a genetic therapy for treating diseases resulting from aberrant signal transduction.

An object of the invention is to provide compounds that desirably influence the signal transduction by the Rho family of Ras-like GTPases.

Another object of the invention is to provide therapeutics for treating diseases resulting from aberrant signal transduction by the Rho family of Ras-like GTPases.

Still another object of the invention is to provide diagnostics and research tools relating to PARG, PTPL1 and the Rho family of Ras-like GTPases. These and other objects will be described in greater detail below.

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Summary of the Invention

The invention provides isolated nucleic acid molecules, unique fragments of those molecules, expression vectors containing the foregoing, and host cells transfected with those molecules. The invention also provides isolated polypeptides and agents which bind such polypeptides, including antibodies. The foregoing can be used in the diagnosis or treatment of conditions characterized by the expression of a PARG nucleic acid or polypeptide. The invention also provides methods for identifying pharmacological agents useful in the diagnosis or treatment of such conditions. Here, we present the cDNA cloning of a PTPL1-associated RhoGAP, PARG, a 150 kDa protein that contains a GAP domain that displays strong activity towards Rho. Furthermore, the C-terminal tail of PARG specifically interacts with the fourth PDZ domain (PDZ4) of PTPL1.

According to one aspect of the invention, an isolated nucleic acid molecule is provided. The molecule hybridizes under stringent conditions to a molecule consisting of the nucleic acid sequence of SEQ ID NO:1. The isolated nucleic acid molecule codes for a GTPase activating polypeptide. The invention further embraces nucleic acid molecules that differ from the foregoing isolated nucleic acid molecules in codon sequence due to the degeneracy of the genetic code. The invention also embraces complements of the foregoing nucleic acids.

In preferred embodiments, the isolated nucleic acid molecule comprises a molecule consisting of the nucleic acid sequence of SEQ ID NO:1. More preferably, the isolated nucleic acid molecule comprises a molecule consisting of nucleotides 184-3966 of SEQ ID NO:1. Preferably the isolated nucleic acid comprises a molecule having a sequence which encodes amino acids 666-853 of SEQ ID NO:2, amino acids 613-652 of SEQ ID NO:2, and/or amino acids 193-509 of SEQ ID NO:2.

According to another aspect of the invention, an isolated nucleic acid molecule is provided. The isolated nucleic acid molecule comprises a molecule consisting of a unique fragment of nucleotides 184-3966 of SEQ ID NO:1 between 12 and 3781 nucleotides in length and complements thereof, provided that the isolated nucleic acid molecule excludes sequences consisting only of SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5 and SEQ ID NO:13. In one embodiment, the isolated nucleic acid molecule consists of between 12 and 32 contiguous nucleotides of SEQ ID NO:1, or complements of such nucleic acid molecules. In preferred embodiments, the unique fragment is at least 14, 15, 16, 17, 18, 20 or 22 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:1, or complements thereof.

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According to another aspect of the invention, an isolated nucleic acid molecule which encodes a PDZ domain binding site is provided, comprising a sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:8 and SEQ ID NO:10, or nucleic acid molecules that differ from the nucleic acid molecules of the group consisting of SEQ ID NO:6, SEQ ID NO:8 and SEQ ID NO:10 in codon sequence due to the degeneracy of the genetic code. Preferably the isolated nucleic acid consists of a molecule having a sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:8 and SEQ ID NO:10.

According to another aspect of the invention, the invention involves expression vectors, and host cells transformed or transfected with such expression vectors, comprising the nucleic acid molecules described above.

According to another aspect of the invention, an isolated polypeptide is provided. The isolated polypeptide is encoded by the isolated nucleic acid molecule of claim 1, 2 or 14, and the polypeptide has GTPase activating activity. In preferred embodiments, the isolated polypeptide comprises a polypeptide having the sequence of amino acids 658-898 of SEQ ID NO:2.

According to a further aspect of the invention, an isolated polypeptide is provided. The isolated polypeptide comprises a polypeptide encoded by a nucleic acid which hybridizes under stringent conditions to nucleotides 2020-2139 of SEQ ID NO:1. In preferred embodiments, the isolated polypeptide comprises a polypeptide having the sequence of amino acids 613-652 of SEQ ID NO:2 is provided. The isolated polypeptide has a Cys-rich domain.

According to another aspect of the invention, an isolated polypeptide is provided. The isolated polypeptide comprises a polypeptide encoded by a nucleic acid which hybridizes under stringent conditions to nucleotides 760-1710 of SEQ ID NO:1. In preferred embodiments, the isolated polypeptide comprises a polypeptide having the sequence of amino acid 193-509 of SEQ ID NO:2 is provided. The isolated polypeptide is a ZPH domain polypeptide.

In other embodiments, the isolated polypeptide consists of a fragment or variant of the foregoing which retains the activity of the foregoing.

According to still another aspect of the invention, an isolated polypeptide is provided. The isolated polypeptide is encoded by a nucleic acid molecule having a sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:8 and SEQ ID NO:10. The isolated polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having the sequence of SEQ ID NO:7, a polypeptide having the sequence of SEQ ID NO:9, and a polypeptide having the sequence of SEQ ID NO:11.

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According to another aspect of the invention, there are provided isolated polypeptides which selectively bind a PARG protein or fragment thereof. The isolated polypeptide in certain embodiments binds to a polypeptide comprising the sequence of amino acids 658-898 of SEQ ID NO:2, amino acids 613-652 of SEQ ID NO:2, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11 or
5 amino acids 193-509 of SEQ ID NO:2. The isolated polypeptide preferably binds to a polypeptide consisting essentially of the sequence of amino acids 658-898 of SEQ ID NO:2, amino acids 613-652 of SEQ ID NO:2, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11 or amino acids 193-509 of SEQ ID NO:2. In preferred embodiments, isolated binding polypeptides include antibodies and fragments of antibodies (e.g., Fab, F(ab)₂, Fd and antibody fragments
10 which include a CDR3 region which binds selectively to the PARG polypeptides of the invention).

The invention provides in another aspect an isolated complex of polypeptides. The isolated complex includes a PTPL1 polypeptide, such a polypeptide including the amino acid sequence of SEQ ID NO:12 bound to a polypeptide as claimed in claim 1. The isolated complex
15 has both PTPL1 phosphatase activity and PARG GAP activity. Preferably the isolated complex consists essentially of the polypeptide of SEQ ID NO:12 and the polypeptide of SEQ ID NO:2.

According to still another aspect of the invention, methods for reducing Rho family GTPase signal transduction in a mammalian cell are provided. The methods involve administering to a mammalian cell an amount of an inhibitor of Rho family GTPase activity
20 effective to reduce Rho family GTPase signal transduction in the mammalian cell. In certain embodiments, the inhibitor is an isolated PARG polypeptide, having Rho GAP activity, encoded by SEQ ID NO:1. In other embodiments, the inhibitor is an isolated complex of polypeptides comprising a polypeptide comprising the amino acid sequence of SEQ ID NO:12 and a polypeptide comprising the amino acid sequence of SEQ ID NO:2.

25 According to still another aspect of the invention, methods for reducing proliferation of a cancer cell are provided. The methods involve administering to a cancer cell an amount of a PARG polypeptide, comprising a polypeptide encoded by the nucleic acid of claim 1, effective to reduce proliferation of the cancer cell.

The invention in a further aspect provides methods for increasing Rho family GTPase
30 signal transduction in a mammalian cell. A dominant negative variant of the polypeptide of SEQ ID NO:2 is administered to the mammalian cell in an amount effective to increase Rho family GTPase signal transduction. Preferably the dominant negative polypeptide includes an

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inactivated GTPase activating domain which contains a deletion or at least one inactivating point mutation.

According to a further aspect of the invention, methods for reducing binding of a protein which includes a PDZ4 domain to a protein which includes a PDZ4 domain binding site are provided. The methods involve contacting the protein which includes PDZ4 domain with an agent which binds to the PDZ4 domain for a time effective to reduce the binding of the protein which includes PDZ4 domain to the protein which includes PDZ4 domain binding site. In certain embodiments the agent is an isolated peptide and includes at its carboxyl terminus the amino acid sequence of SEQ ID NO:7. The isolated peptide can include conservative substitutions of the amino acid sequence of SEQ ID NO:7, excepting the terminal valine. In preferred embodiments the amino acid sequence of the peptide is selected from the group consisting of SEQ ID NO:7, SEQ ID NO:9 and SEQ ID NO:11. In other embodiments the agent is an antibody which binds to the PDZ4 domain, preferably a monoclonal antibody. In some embodiments, methods provide inhibiting binding of a protein which includes a PDZ4 domain and a protein which includes a PDZ4 domain binding site in a mammalian cell. Such methods involve contacting the mammalian cell with an agent which binds to the PDZ4 domain for a time effective to reduce the binding of the protein which includes PDZ4 domain to the protein which includes PDZ4 domain binding site.

The invention in another aspect provides methods of modulating mast cell secretion in a subject. The methods include administering to the subject in need of such treatment an amount of a modulator of PARG GTPase activating activity effective to modulate mast cell secretion in the subject.

The invention in still another aspect provides compositions comprising a PARG polypeptide which has GTPase activating activity, a complex of such a PARG polypeptide and PTPL1 phosphatase, or a peptide agent which binds to a PDZ4 domain and which includes the sequence of SEQ ID NO:7, and a pharmaceutically acceptable carrier.

The invention in a further aspect involves a method for decreasing PARG GTPase activating activity in a subject. An agent that selectively binds to an isolated nucleic acid molecule of the invention or an expression product thereof is administered to a subject in need of such treatment, in an amount effective to decrease PARG GTPase activating activity in the subject. Preferred agents are antisense nucleic acids, including modified nucleic acids, and polypeptides.

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According to another aspect of the invention, methods are provided for identifying lead compounds for a pharmacological agent useful in the diagnosis or treatment of disease associated with PARG GTPase activating activity or with PARG binding to a protein containing a PDZ4 domain. The methods involve forming a mixture of a PARG polypeptide or fragment thereof containing a GTPase activating domain or a PDZ4 domain binding site, a protein which interacts with the foregoing GTPase activating domain or PDZ4 domain binding site, and a candidate pharmacological agent. The mixture is incubated under conditions which, in the absence of the candidate pharmacological agent, permit a first amount of specific activation of the GTPase by the PARG GTPase activating domain or permit a first amount of selective binding of the protein containing a PDZ4 domain by the PDZ4 domain binding site. A test amount of the specific activation of the GTPase by the PARG GTPase activating domain or the selective binding of the protein containing a PDZ4 domain by the PDZ4 domain binding site then is detected. Detection of an increase in the foregoing activities in the presence of the candidate pharmacological agent indicates that the candidate pharmacological agent is a lead compound for a pharmacological agent which increases specific activation of the GTPase by the PARG GTPase activating domain or selective binding of the protein containing a PDZ4 domain by the PDZ4 domain binding site. Detection of a decrease in the foregoing activities in the presence of the candidate pharmacological agent indicates that the candidate pharmacological agent is a lead compound for a pharmacological agent which decreases specific activation of the GTPase by the PARG GTPase activating domain or selective binding of the protein containing a PDZ4 domain by the PDZ4 domain binding site. Where the activity tested is specific activation of the GTPase, the protein which interacts with the GTPase activating domain preferably is Rho. Where the activity tested is selective binding of a PDZ4 domain, the protein which interacts with the PDZ4 domain binding site preferably is PTPL1.

The invention also contemplates specifically the use of the foregoing compositions in the manufacture of a medicament, particularly medicaments for treating conditions characterized by aberrant Rho family protein signal transduction, cell proliferation and/or mast cell secretion.

These and other objects of the invention will be described in further detail in connection with the detailed description of the invention.

Brief Description of the Drawings

Figure 1 is a representation of the production GST-PDZ fusion proteins. (A) Schematic

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illustration of the GST-PDZ fusion proteins showing the domain structure of PTPL1 and the design of PTPL1 -derived GST-PDZ fusion proteins (B) Expression of GST-PDZ fusion proteins.

5 Figure 2 shows the interaction of GST-PDZ fusion proteins with components in cell lysate.

Figure 3 depicts the structure of PARG protein. (A) Deduced amino acid sequence of PARG. (B) Comparison of amino acid sequences of ZPH regions found in PARG and in the gene product of the *C. elegans* gene ZK669.1a. (C) Schematic diagram illustrating the domain structure of PARG and ZK669.1a.

10 Figure 4 shows Northern blot analysis of expression of PARG mRNA in different human tissues.

Figure 5 shows an analysis of the GAP activity of PARG. (A) Expression of the GAP domain of PARG as a GST fusion protein. Rho (B), Rac (C), and Cdc42 (D) loaded with γ -³²P-GTP were incubated with 1 nM (open circles), 20 nM (filled circles) of the GAP domain of PARG expressed as a GST fusion protein, or 1 00 nM GST (squares) as a control, for different
15 time periods at 30°C.

Figure 6 shows binding of GST-PDZ fusion proteins to a C-terminal PARG peptide.

Brief Description of the Sequences

20 SEQ ID NO:1 is the nucleotide sequence of the PARG cDNA.

SEQ ID NO:2 is the amino acid sequence of the translation product of the PARG cDNA, including a RhoGAP domain at amino acids 666-853, a cysteine-rich domain at amino acids 613-652, a ZPH domain at amino acids 193-509 of SEQ ID NO:2, and a carboxyl-terminal PDZ domain binding site.

25 SEQ ID NO:3 is the nucleotide sequence of the expressed sequence tag identified by GenBank accession number T32345.

SEQ ID NO:4 is the nucleotide sequence of the expressed sequence tag identified by GenBank accession number Z28937.

30 SEQ ID NO:5 is the nucleotide sequence of the expressed sequence tag identified by GenBank accession number Z28520.

SEQ ID NO:6 is the nucleotide sequence encoding the PARG PDZ domain binding site which consists of 4 amino acids.

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SEQ ID NO:7 is the amino acid sequence of the PARG PDZ domain binding site which consists of 4 amino acids.

SEQ ID NO:8 is the nucleotide sequence encoding the PARG PDZ domain binding site which consists of 5 amino acids.

5 SEQ ID NO:9 is the amino acid sequence of the PARG PDZ domain binding site which consists of 5 amino acids.

SEQ ID NO:10 is the nucleotide sequence encoding the PARG PDZ domain binding site which consists of 6 amino acids.

10 SEQ ID NO:11 is the amino acid sequence of the PARG PDZ domain binding site which consists of 6 amino acids.

SEQ ID NO:12 is the amino acid sequence of the PTPL1 phosphatase.

SEQ ID NO:13 is the nucleotide sequence of the expressed sequence tag identified by GenBank accession number T32506.

15

Detailed Description of the Invention

The present invention in one aspect involves the cloning of a cDNA encoding a PARG GTPase activating protein. The sequence of the human gene is presented as SEQ ID NO:1, and the predicted amino acid sequence of this gene's protein product is presented as SEQ ID NO:2. Analysis of the sequence by comparison to nucleic acid and protein databases determined that
20 PARG has several domains in addition to the GAP domain. These include a cysteine-rich domain located directly N-terminal of the GAP domain, a ZPH domain similar to the ZK669.1 gene product of *C. elegans* (Wilson et al., *Nature* 368: 32-38, 1994), and a PDZ domain binding site.

The GAP activity of PARG was determined as reported in Example 7 below. The GAP
25 activity of this protein is strongest on Rho GTPase *in vitro*. GAP activities were also detected on Rac and Cdc42 *in vitro*. Because these activities on Rac and Cdc42 were observed at higher PARG concentrations than needed for Rho GAP activity, it is likely that Rho is the preferred *in vivo* target of PARG.

A cysteine-rich domain is located directly N-terminal of the GAP domain of PARG. This
30 domain has been identified in various proteins including most PKC isoforms (which have two copies each of the domain), the protooncogene products Vav and Raf, diacylglycerol kinase and chimaerins (reviewed by Newton, *Curr. Biol.* 5: 973-976, 1995). The cysteine-rich domain has

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been shown to bind Zn^{2+} (Ahmed *et al.*, *Biochem J.* 280: 233-241, 1991), and the domains found in PKCs and in chimaerins also bind phorbol esters and diacylglycerol (Ahmed *et al.*, 1991; Ono *et al.*, *Proc. Natl. Acad. Sci. USA* 86: 4868-4871, 1989). Generation of diacylglycerol or addition of phorbol ester increase the affinity of PKC molecules for membranes, and the resulting translocation of PKC from the cytosol to the plasma membrane is likely to involve interactions between the cysteine-rich domains and membrane phospholipids (Newton, 1995; Zhang *et al.*, *Cell* 81: 917-924, 1995). The cysteine-rich domain of PARG may mediate regulatable binding to the membrane and could possibly also be involved in regulation of the GAP activity. Thus, a function of the cysteine-rich domain of PARG may be analogous to a function of $n(\alpha)$ -chimaerin, a Rac-specific GAP, which contains a copy of a homologous cysteine-rich domain; it has been shown that phospholipids and phorbol esters regulate the GAP activity of $n(\alpha)$ -chimaerin (Ahmed *et al.*, *J. Biol. Chem.* 268: 10709-10712, 1993).

In the N-terminal part of PARG, a region of about 300 amino acid residues with similarity (27 % identity) to the gene product of the *C. elegans* gene ZK669.1a was identified, and denoted ZPH region. The overall domain structure of the ZK669.1a gene product is similar to PARG and it is possible that PARG is the human homolog of the *C. elegans* ZK669.1a gene product. However, the RhoGAP domain and the cysteine-rich domain of the ZK669.1a gene product is not significantly more similar to PARG (29 % identity within the RhoGAP domains, 24 % identity within the cysteine-rich domains) compared to other human proteins containing these domains (24-31 % identity within the RhoGAP domains and 16-27 % identity within the cysteine-rich domains).

PDZ domains have been identified in a diverse set of proteins (Ponting and Phillips, *Trends Biochem. Sci.* 20: 102-103, 1995). These proteins seem to be involved in signal transduction, and many of them, if not all, are found in structures at the plasma membrane. The size of the PDZ domain of about 90 amino acid residues, and its appearance in signal transduction proteins suggested that it, like SH2 and SH3 domains, can mediate direct interactions with other molecules. We have shown that PARG binds specifically to PDZ4 of PTPL1 and that the binding-site for binding to PDZ 4 resides in the four most C-terminal amino acid residues of PARG. PDZ domains can bind strongly to a short peptide of only four amino acid residues, and the carboxy-group and the side chain of the C-terminal valine residue is important for binding. The crystal structure of the third PDZ domain of PSD-95 binding to a peptide (Doyle *et al.*, 1996; Morais Cabral *et al.*, 1996) confirms these results and shows that the

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last four C-terminal amino acid residues of the peptide bind in a cleft of the domain with the C-terminal valine buried in a shallow pocket. Thus, the PDZ domain functions as a C-terminal peptide binding module. Because PDZ 4 binds to PARG, a complex between PTPL1, PARG, and Rho can be formed. Protein tyrosine kinases have been implicated to act upstream and downstream of Rho (Nobes and Hall, *J. Cell Sci.* 108:225-233, 1995; Ridley, *BioEssays* 16:321-327, 1994). Thus, PTPL1 can function as a negative regulator of kinases in the Rho signal pathway, and in complex with PARG, which inactivates Rho itself, it can be a powerful inhibitor of Rho signals.

The invention thus involves in one aspect PARG polypeptides, genes encoding those polypeptides, functional modifications and variants of the foregoing, useful fragments of the foregoing, as well as therapeutics relating thereto.

Homologs and alleles of the PARG nucleic acids of the invention can be identified by conventional techniques. Thus, an aspect of the invention is those nucleic acid sequences which code for PARG polypeptides and which hybridize to a nucleic acid molecule consisting of the coding region of SEQ ID NO:1, under stringent conditions. The term "stringent conditions" as used herein refers to parameters with which the art is familiar. Nucleic acid hybridization parameters may be found in references which compile such methods, e.g. *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989, or *Current Protocols in Molecular Biology*, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. More specifically, stringent conditions, as used herein, refers, for example, to hybridization at 65°C in hybridization buffer (3.5 x SSC, 0.02% Ficoll, 0.02% polyvinyl pyrrolidone, 0.02% Bovine Serum Albumin, 2.5mM NaH₂PO₄(pH7), 0.5% SDS, 2mM EDTA). SSC is 0.15M sodium chloride/0.15M sodium citrate, pH7; SDS is sodium dodecyl sulphate; and EDTA is ethylenediaminetetracetic acid. After hybridization, the membrane upon which the DNA is transferred is washed at 2 x SSC at room temperature and then at 0.1 x SSC/0.1 x SDS at temperatures up to 65°C.

There are other conditions, reagents, and so forth which can be used, which result in a similar degree of stringency. The skilled artisan will be familiar with such conditions, and thus they are not given here. It will be understood, however, that the skilled artisan will be able to manipulate the conditions in a manner to permit the clear identification of homologs and alleles of PARG nucleic acids of the invention. The skilled artisan also is familiar with the methodology for screening cells and libraries for expression of such molecules which then are

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routinely isolated, followed by isolation of the pertinent nucleic acid molecule and sequencing.

In general homologs and alleles typically will share at least 40% nucleotide identity and/or at least 50% amino acid identity to SEQ ID NO:1 and SEQ ID NO:2, respectively, in some instances will share at least 50% nucleotide identity and/or at least 65% amino acid identity and in still other instances will share at least 60% nucleotide identity and/or at least 75% amino acid identity. Watson-Crick complements of the foregoing nucleic acids also are embraced by the invention.

In screening for PARG proteins, a Southern blot may be performed using the foregoing conditions, together with a radioactive probe. After washing the membrane to which the DNA is finally transferred, the membrane can be placed against X-ray film to detect the radioactive signal.

The invention also includes degenerate nucleic acids which include alternative codons to those present in the native materials. For example, serine residues are encoded by the codons TCA, AGT, TCC, TCG, TCT and AGC. Each of the six codons is equivalent for the purposes of encoding a serine residue. Thus, it will be apparent to one of ordinary skill in the art that any of the serine-encoding nucleotide triplets may be employed to direct the protein synthesis apparatus, *in vitro* or *in vivo*, to incorporate a serine residue into an elongating PARG polypeptide. Similarly, nucleotide sequence triplets which encode other amino acid residues include, but are not limited to, CCA, CCC, CCG and CCT (proline codons); CGA, CGC, CGG, CGT, AGA and AGG (arginine codons); ACA, ACC, ACG and ACT (threonine codons); AAC and AAT (asparagine codons); and ATA, ATC and ATT (isoleucine codons). Other amino acid residues may be encoded similarly by multiple nucleotide sequences. Thus, the invention embraces degenerate nucleic acids that differ from the biologically isolated nucleic acids in codon sequence due to the degeneracy of the genetic code.

The invention also provides isolated unique fragments of SEQ ID NO:1 or complements of SEQ ID NO:1. A unique fragment is one that is a 'signature' for the larger nucleic acid. It, for example, is long enough to assure that its precise sequence is not found in molecules outside of the PARG nucleic acids defined above. Unique fragments can be used as probes in Southern blot assays to identify such nucleic acids, or can be used in amplification assays such as those employing PCR. As known to those skilled in the art, large probes such as 200 nucleotides or more are preferred for certain uses such as Southern blots, while smaller fragments will be preferred for uses such as PCR. Unique fragments also can be used to produce fusion proteins

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for generating antibodies or determining binding of the polypeptide fragments, as demonstrated in the Examples, or for generating immunoassay components. Likewise, unique fragments can be employed to produce nonfused fragments of the PARG polypeptides, useful, for example, in the preparation of antibodies, in immunoassays, and as a competitive binding partner of the

5 PTPL1 phosphatase and/or other polypeptides which bind to the PARG polypeptides, for example, in therapeutic applications. Unique fragments further can be used as antisense molecules to inhibit the expression of PARG nucleic acids and polypeptides, particularly for therapeutic purposes as described in greater detail below.

As will be recognized by those skilled in the art, the size of the unique fragment will

10 depend upon its conservancy in the genetic code. Thus, some regions of SEQ ID NO:1 and its complement will require longer segments to be unique while others will require only short segments, typically between 12 and 32 nucleotides (e.g. 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 and 32 bases long). Excluding nucleic acid molecules consisting completely of the nucleotide sequence of SEQ ID NO:3 (GenBank accession number

15 T32345), SEQ ID NO:4 (GenBank accession number Z28937), SEQ ID NO:5 (GenBank accession number Z28520) or SEQ ID NO:13 (GenBank accession number T32506) which overlaps SEQ ID NO:1, virtually any segment of the region of SEQ ID NO:1 beginning at nucleotide 184 and ending at nucleotide 3966, or complements thereof, that is 18 or more nucleotides in length will be unique. A fragment which is completely composed of the sequence

20 of SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5 or SEQ ID NO:13 is one which does not include any of the nucleotides unique to PARG. Preferred longer unique fragments include those which are at least 50, 100, 150, 200, 250, 300, or 500 nucleotide in length. Particularly preferred are those unique fragments drawn completely from the portion of SEQ ID NO:3 which is not overlapped by the sequence of SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5 or SEQ ID NO:13.

25 Those skilled in the art are well versed in methods for selecting such sequences, typically on the basis of the ability of the unique fragment to selectively distinguish the sequence of interest from non-PARG nucleic acids. A comparison of the sequence of the fragment to those on known data bases typically is all that is necessary, although *in vitro* confirmatory hybridization and sequencing analysis may be performed.

30 As mentioned above, the invention embraces antisense oligonucleotides that selectively bind to a nucleic acid molecule encoding a PARG polypeptide, to decrease GTPase activation by PARG or phosphatase binding by PARG. This is desirable in virtually any medical condition

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wherein a reduction in GTPase activating activity of PARG is desirable, including to reduce Rho family protein signal transduction, or wherein a reduction in phosphatase binding by PARG is desirable. Antisense molecules, in this manner, can be used to slow down or arrest the proliferation of cancer cells *in vivo*.

5 As used herein, the term "antisense oligonucleotide" or "antisense" describes an oligonucleotide that is an oligoribonucleotide, oligodeoxyribonucleotide, modified oligoribonucleotide, or modified oligodeoxyribonucleotide which hybridizes under physiological conditions to DNA comprising a particular gene or to an mRNA transcript of that gene and, thereby, inhibits the transcription of that gene and/or the translation of that mRNA. The
10 antisense molecules are designed so as to interfere with transcription or translation of a target gene upon hybridization with the target gene or transcript. Those skilled in the art will recognize that the exact length of the antisense oligonucleotide and its degree of complementarity with its target will depend upon the specific target selected, including the sequence of the target and the particular bases which comprise that sequence. It is preferred that the antisense oligonucleotide
15 be constructed and arranged so as to bind selectively with the target under physiological conditions, i.e., to hybridize substantially more to the target sequence than to any other sequence in the target cell under physiological conditions. Based upon SEQ ID NO:1, or upon allelic or homologous genomic and/or cDNA sequences, one of skill in the art can easily choose and synthesize any of a number of appropriate antisense molecules for use in accordance with the
20 present invention. In order to be sufficiently selective and potent for inhibition, such antisense oligonucleotides should comprise at least 10 and, more preferably, at least 15 consecutive bases which are complementary to the target, although in certain cases modified oligonucleotides as short as 7 bases in length have been used successfully as antisense oligonucleotides (Wagner et al., *Nature Biotechnol.* 14:840-844, 1996). Most preferably, the antisense oligonucleotides
25 comprise a complementary sequence of 20-30 bases. Although oligonucleotides may be chosen which are antisense to any region of the gene or mRNA transcripts, in preferred embodiments the antisense oligonucleotides correspond to N-terminal or 5' upstream sites such as translation initiation, transcription initiation or promoter sites. In addition, 3'-untranslated regions may be targeted. Targeting to mRNA splicing sites has also been used in the art but may be less
30 preferred if alternative mRNA splicing occurs. In addition, the antisense is targeted, preferably, to sites in which mRNA secondary structure is not expected (see, e.g., Sainio et al., *Cell Mol. Neurobiol.* 14(5):439-457, 1994) and at which proteins are not expected to bind. Finally,

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although, SEQ ID NO:1 discloses a cDNA sequence, one of ordinary skill in the art may easily derive the genomic DNA corresponding to the cDNA of SEQ ID NO:1. Thus, the present invention also provides for antisense oligonucleotides which are complementary to the genomic DNA corresponding to SEQ ID NO:1. Similarly, antisense to allelic or homologous cDNAs and
5 genomic DNAs are enabled without undue experimentation.

In one set of embodiments, the antisense oligonucleotides of the invention may be composed of "natural" deoxyribonucleotides, ribonucleotides, or any combination thereof. That is, the 5' end of one native nucleotide and the 3' end of another native nucleotide may be covalently linked, as in natural systems, via a phosphodiester internucleoside linkage. These
10 oligonucleotides may be prepared by art recognized methods which may be carried out manually or by an automated synthesizer. They also may be produced recombinantly by vectors.

In preferred embodiments, however, the antisense oligonucleotides of the invention also may include "modified" oligonucleotides. That is, the oligonucleotides may be modified in a number of ways which do not prevent them from hybridizing to their target but which enhance
15 their stability or targeting or which otherwise enhance their therapeutic effectiveness.

The term "modified oligonucleotide" as used herein describes an oligonucleotide in which (1) at least two of its nucleotides are covalently linked via a synthetic internucleoside linkage (i.e., a linkage other than a phosphodiester linkage between the 5' end of one nucleotide and the 3' end of another nucleotide) and/or (2) a chemical group not normally associated with
20 nucleic acids has been covalently attached to the oligonucleotide. Preferred synthetic internucleoside linkages are phosphorothioates, alkylphosphonates, phosphorodithioates, phosphate esters, alkylphosphonothioates, phosphoramidates, carbamates, carbonates, phosphate triesters, acetamidates, carboxymethyl esters and peptides.

The term "modified oligonucleotide" also encompasses oligonucleotides with a
25 covalently modified base and/or sugar. For example, modified oligonucleotides include oligonucleotides having backbone sugars which are covalently attached to low molecular weight organic groups other than a hydroxyl group at the 3' position and other than a phosphate group at the 5' position. Thus modified oligonucleotides may include a 2'-O-alkylated ribose group. In addition, modified oligonucleotides may include sugars such as arabinose instead of ribose. The
30 present invention, thus, contemplates pharmaceutical preparations containing modified antisense molecules that are complementary to and hybridizable with, under physiological conditions, nucleic acids encoding PARG polypeptides, together with pharmaceutically acceptable carriers.

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Antisense oligonucleotides may be administered as part of a pharmaceutical composition. Such a pharmaceutical composition may include the antisense oligonucleotides in combination with any standard physiologically and/or pharmaceutically acceptable carriers which are known in the art. The compositions should be sterile and contain a therapeutically effective amount of the antisense oligonucleotides in a unit of weight or volume suitable for administration to a patient. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredients. The term "physiologically acceptable" refers to a non-toxic material that is compatible with a biological system such as a cell, cell culture, tissue, or organism. The characteristics of the carrier will depend on the route of administration. Physiologically and pharmaceutically acceptable carriers include diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials which are well known in the art.

As used herein, a "vector" may be any of a number of nucleic acids into which a desired sequence may be inserted by restriction and ligation for transport between different genetic environments or for expression in a host cell. Vectors are typically composed of DNA although RNA vectors are also available. Vectors include, but are not limited to, plasmids, phagemids and virus genomes. A cloning vector is one which is able to replicate in a host cell, and which is further characterized by one or more endonuclease restriction sites at which the vector may be cut in a determinable fashion and into which a desired DNA sequence may be ligated such that the new recombinant vector retains its ability to replicate in the host cell. In the case of plasmids, replication of the desired sequence may occur many times as the plasmid increases in copy number within the host bacterium or just a single time per host before the host reproduces by mitosis. In the case of phage, replication may occur actively during a lytic phase or passively during a lysogenic phase. An expression vector is one into which a desired DNA sequence may be inserted by restriction and ligation such that it is operably joined to regulatory sequences and may be expressed as an RNA transcript. Vectors may further contain one or more marker sequences suitable for use in the identification of cells which have or have not been transformed or transfected with the vector. Markers include, for example, genes encoding proteins which increase or decrease either resistance or sensitivity to antibiotics or other compounds, genes which encode enzymes whose activities are detectable by standard assays known in the art (e.g., β -galactosidase or alkaline phosphatase), and genes which visibly affect the phenotype of transformed or transfected cells, hosts, colonies or plaques (e.g., green fluorescent protein).

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Preferred vectors are those capable of autonomous replication and expression of the structural gene products present in the DNA segments to which they are operably joined.

As used herein, a coding sequence and regulatory sequences are said to be "operably" joined when they are covalently linked in such a way as to place the expression or transcription of the coding sequence under the influence or control of the regulatory sequences. If it is desired that the coding sequences be translated into a functional protein, two DNA sequences are said to be operably joined if induction of a promoter in the 5' regulatory sequences results in the transcription of the coding sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the coding sequences, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a promoter region would be operably joined to a coding sequence if the promoter region were capable of effecting transcription of that DNA sequence such that the resulting transcript might be translated into the desired protein or polypeptide.

The precise nature of the regulatory sequences needed for gene expression may vary between species or cell types, but shall in general include, as necessary, 5' non-transcribed and 5' non-translated sequences involved with the initiation of transcription and translation respectively, such as a TATA box, capping sequence, CAAT sequence, and the like. Especially, such 5' non-transcribed regulatory sequences will include a promoter region which includes a promoter sequence for transcriptional control of the operably joined gene. Regulatory sequences may also include enhancer sequences or upstream activator sequences as desired. The vectors of the invention may optionally include 5' leader or signal sequences. The choice and design of an appropriate vector is within the ability and discretion of one of ordinary skill in the art.

Expression vectors containing all the necessary elements for expression are commercially available and known to those skilled in the art. See, e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989. Cells are genetically engineered by the introduction into the cells of heterologous DNA (RNA) encoding PARC polypeptide or fragment or variant thereof. That heterologous DNA (RNA) is placed under operable control of transcriptional elements to permit the expression of the heterologous DNA in the host cell.

Preferred systems for mRNA expression in mammalian cells are those such as pRc/CMV (available from Invitrogen, Carlsbad, CA) that contain a selectable marker such as a gene that

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confers G418 resistance (which facilitates the selection of stably transfected cell lines) and the human cytomegalovirus (CMV) enhancer-promoter sequences. Additionally, suitable for expression in primate or canine cell lines is the pCEP4 vector (Invitrogen), which contains an Epstein Barr virus (EBV) origin of replication, facilitating the maintenance of plasmid as a multicopy extrachromosomal element. Another expression vector is the pEF-BOS plasmid containing the promoter of polypeptide Elongation Factor 1 α , which stimulates efficiently transcription *in vitro*. The plasmid is described by Mishizuma and Nagata (*Nuc. Acids Res.* 18:5322, 1990), and its use in transfection experiments is disclosed by, for example, Demoulin (*Mol. Cell. Biol.* 16:4710-4716, 1996). Still another preferred expression vector is an adenovirus, described by Stratford-Perricaudet, which is defective for E1 and E3 proteins (*J. Clin. Invest.* 90:626-630, 1992). The use of the adenovirus as an Adeno.P1A recombinant is disclosed by Warnier et al., in intradermal injection in mice for immunization against P1A (*Int. J. Cancer*, 67:303-310, 1996).

The invention also embraces so-called expression kits, which allow the artisan to prepare a desired expression vector or vectors. Such expression kits include at least separate portions of each of the previously discussed coding sequences. Other components may be added, as desired, as long as the previously mentioned sequences, which are required, are included.

The invention also permits the construction of PARG gene "knock-outs" in cells and in animals, providing materials for studying certain aspects of GTPase activating activity and signal transduction.

The invention also provides isolated polypeptides, which include the polypeptide of SEQ ID NO:2 and unique fragments of SEQ ID NO:2, particularly amino acids 193-509, 613-652 and 658-898 of SEQ ID NO:2, as well as the carboxyl terminal 4, 5 or 6 amino acids of SEQ ID NO:2. Such polypeptides are useful, for example, alone or as fusion proteins to generate antibodies, as a components of an immunoassay.

A unique fragment of an PARG polypeptide, in general, has the features and characteristics of unique fragments as discussed above in connection with nucleic acids. As will be recognized by those skilled in the art, the size of the unique fragment will depend upon factors such as whether the fragment constitutes a portion of a conserved protein domain. Thus, some regions of amino acids 658-898 of SEQ ID NO:2, amino acid residues 613-652 of SEQ ID NO:2 and amino acid residues of 193-509 SEQ ID NO:2, will require longer segments to be unique while others will require only short segments, typically between 5 and 12 amino acids (e.g. 5, 6,

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7, 8, 9, 10, 11 and 12 amino acids long). Virtually any segment of amino acids 658-898 of SEQ ID NO:2, amino acid residues 613-652 of SEQ ID NO:2 and amino acid residues of 193-509 SEQ ID NO:2, that is 10 or more amino acids in length will be unique.

Unique fragments of a polypeptide preferably are those fragments which retain a distinct functional capability of the polypeptide. Functional capabilities which can be retained in a unique fragment of a polypeptide include interaction with antibodies, interaction with other polypeptides (such as Rho) or fragments thereof, selective binding of nucleic acids or proteins (such as PTPL1), and enzymatic activity. Those skilled in the art are well versed in methods for selecting unique amino acid sequences, typically on the basis of the ability of the unique fragment to selectively distinguish the sequence of interest from non-family members. A comparison of the sequence of the fragment to those on known data bases typically is all that is necessary.

The invention embraces variants of the PARG polypeptides described above. As used herein, a "variant" of a PARG polypeptide is a polypeptide which contains one or more modifications to the primary amino acid sequence of a PARG polypeptide. Modifications which create a PARG variant can be made to a PARG polypeptide 1) to reduce or eliminate an activity of a PARG polypeptide, such as PTPL1 binding or GAP activity for Rho GTPase; 2) to enhance a property of a PARG polypeptide, such as protein stability in an expression system or the stability of protein-protein binding; or 3) to provide a novel activity or property to a PARG polypeptide, such as addition of an antigenic epitope or addition of a detectable moiety. Modifications to a PARG polypeptide are typically made to the nucleic acid which encodes the PARG polypeptide, and can include deletions, point mutations, truncations, amino acid substitutions and additions of amino acids or non-amino acid moieties. Alternatively, modifications can be made directly to the polypeptide, such as by cleavage, addition of a linker molecule, addition of a detectable moiety, such as biotin, addition of a fatty acid, and the like. Modifications also embrace fusion proteins comprising all or part of the PARG amino acid sequence.

In general, variants include PARG polypeptides which are modified specifically to alter a feature of the polypeptide unrelated to its physiological activity. For example, cysteine residues can be substituted or deleted to prevent unwanted disulfide linkages. Similarly, certain amino acids can be changed to enhance expression of a PARG polypeptide by eliminating proteolysis by proteases in an expression system (e.g., dibasic amino acid residues in yeast expression

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systems in which KEX2 protease activity is present).

Mutations of a nucleic acid which encode a PARG polypeptide preferably preserve the amino acid reading frame of the coding sequence, and preferably do not create regions in the nucleic acid which are likely to hybridize to form secondary structures, such as hairpins or loops, which can be deleterious to expression of the variant polypeptide.

Mutations can be made by selecting an amino acid substitution, or by random mutagenesis of a selected site in a nucleic acid which encodes the polypeptide. Variant polypeptides are then expressed and tested for one or more activities to determine which mutation provides a variant polypeptide with the desired properties. Further mutations can be made to variants (or to non-variant PARG polypeptides) which are silent as to the amino acid sequence of the polypeptide, but which provide preferred codons for translation in a particular host. The preferred codons for translation of a nucleic acid in, e.g., *E. coli*, are well known to those of ordinary skill in the art. Still other mutations can be made to the noncoding sequences of a PARG gene or cDNA clone to enhance expression of the polypeptide. The activity of variants of PARG polypeptides can be tested by cloning the gene encoding the variant PARG polypeptide into a bacterial or mammalian expression vector, introducing the vector into an appropriate host cell, expressing the variant PARG polypeptide, and testing for a functional capability of the PARG polypeptides as disclosed herein. For example, the variant PARG polypeptide can be tested for Rho GAP activity as disclosed in Example 7, or for PDZ binding as disclosed in other Examples herein. Preparation of other variant polypeptides may favor testing of other activities, as will be known to one of ordinary skill in the art.

The skilled artisan will also realize that conservative amino acid substitutions may be made in PARG polypeptides to provide functionally equivalent variants of the foregoing polypeptides, i.e., the variants retain the functional capabilities of the PARG polypeptides. As used herein, a "conservative amino acid substitution" refers to an amino acid substitution which does not alter the relative charge or size characteristics of the protein in which the amino acid substitution is made. Variants can be prepared according to methods for altering polypeptide sequence known to one of ordinary skill in the art such as are found in references which compile such methods, e.g. *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989, or *Current Protocols in Molecular Biology*, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. Exemplary functionally equivalent variants of the PARG polypeptides include conservative

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amino acid substitutions of SEQ ID NO:2, particularly conservative substitutions of amino acids other than 193-509, 613-652 or 658-898 of SEQ ID NO:2. However, conservative substitutions of amino acids 193-509, 613-652 or 658-898 of SEQ ID NO:2 can be made as well.

Conservative substitutions of amino acids include substitutions made amongst amino acids

5 within the following groups: (a) M, I, L, V; (b) F, Y, W; (c) K, R, H; (d) A, G; (e) S, T; (f) Q, N; and (g) E, D. Changes to the carboxyl terminal valine of the PARG PDZ domain binding site are not preferred for retention of maximal binding activity.

Conservative amino-acid substitutions in the amino acid sequence of PARG polypeptides to produce functionally equivalent variants of PARG polypeptides typically are made by
10 alteration of the nucleic acid encoding PARG polypeptides (SEQ ID NO:1). Such substitutions can be made by a variety of methods known to one of ordinary skill in the art. For example, amino acid substitutions may be made by PCR-directed mutation, site-directed mutagenesis according to the method of Kunkel (Kunkel, *Proc. Nat. Acad. Sci. U.S.A.* 82: 488-492, 1985), or by chemical synthesis of a gene encoding a PARG polypeptide. Where amino acid substitutions
15 are made to a small unique fragment of a PARG polypeptide, such as a PDZ-domain binding site peptide, the substitutions can be made by directly synthesizing the peptide. The activity of functionally equivalent fragments of PARG polypeptides can be tested by cloning the gene encoding the altered PARG polypeptide into a bacterial or mammalian expression vector, introducing the vector into an appropriate host cell, expressing the altered PARG polypeptide,
20 and testing for a functional capability of the PARG polypeptides as disclosed herein. Peptides which are chemically synthesized can be tested directly for function, e.g., for binding to a PDZ 4 domain of PTPL1.

The invention as described herein has a number of uses, some of which are described elsewhere herein. First, the invention permits isolation of the PARG protein molecule (SEQ ID
25 NO:2). A variety of methodologies well-known to the skilled practitioner can be utilized to obtain isolated PARG molecules. The polypeptide may be purified from cells which naturally produce the polypeptide by chromatographic means or immunological recognition.

Alternatively, an expression vector may be introduced into cells to cause production of the polypeptide. In another method, mRNA transcripts may be microinjected or otherwise
30 introduced into cells to cause production of the encoded polypeptide. Translation of mRNA in cell-free extracts such as the reticulocyte lysate system also may be used to produce polypeptide. Those skilled in the art also can readily follow known methods for isolating PARG polypeptides.

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These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography and immune-affinity chromatography.

The isolation of the PARG gene also makes it possible for the artisan to diagnose a disorder characterized by expression of PARG. These methods involve determining expression
5 of the PARG gene, and/or PARG polypeptides derived therefrom. In the former situation, such determinations can be carried out via any standard nucleic acid determination assay, including the polymerase chain reaction as exemplified in the examples below, or assaying with labeled hybridization probes.

The invention also makes it possible isolate proteins having a PDZ4 domain by the
10 binding of such proteins to the PDZ domain binding site disclosed herein. The identification of the PDZ domain binding site also permits one of skill in the art to block the binding of a protein having a PDZ4 domain, such as PTPL1, with a binding partner having a PDZ4 domain binding site, such as PARG. Binding of the proteins can be effected by introducing into a biological system in which the proteins bind (e.g., a cell) a polypeptide including a PDZ domain binding
15 site in an amount sufficient to block the binding. The identification of the PDZ4 domain binding site in PARG also enables one of skill in the art to prepare modified proteins, using standard recombinant DNA techniques, which can bind to proteins containing a PDZ4 domain. For example, when one desires to target a certain protein to the inner membrane surface where proteins containing a PDZ domain, such as PTPL1, are localized, one can prepare a fusion
20 polypeptide of the protein and the PDZ4 domain binding site. Preferably, the PDZ domain binding site is fused to the carboxy terminus of the protein. Additional uses are described further herein.

The invention further provides methods for reducing or increasing Rho family signal transduction in a cell. Such methods are useful *in vitro* for altering the Rho signal transduction,
25 for example, in testing compounds for potential to block aberrant Rho signal transduction. *In vivo*, such methods are useful for modulating actin polymerization, cell proliferation and release of secretory granules from mast cells (see, e.g., Price et al., *Curr. Biol.* 5:68-73, 1995), e.g., to treat allergy. Increasing Rho signal transduction in a cell by, e.g., introducing a dominant negative PARG polypeptide in the cell, can be used to provide a model system for testing the
30 effects of putative inhibitors of Rho signal transduction. Such methods also are useful in the treatment of conditions which result from excessive or deficient Rho signal transduction. Rho signal transduction can be measured by studying actin reorganization or by measuring the ratio

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of Rho-bound GTP/GDP. Various modulators of PARG GTPase activating activity can be screened for effects on Rho signal transduction using the methods disclosed herein. The skilled artisan can first determine the modulation of a PARG activity, such as GTPase activating activity, and then apply such a modulator to a target cell or subject and assess the effect on the target cell or subject. For example, in screening for modulators of PARG useful in the treatment of mast cell secretion, mast cells in culture can be contacted with PARG modulators and the increase or decrease of secretory granule release by the mast cells can be determined according to standard procedures. PARG activity modulators can be assessed for their effects on other Rho signal transduction downstream effects by similar methods in other cell types.

The invention also provides, in certain embodiments, "dominant negative" polypeptides derived from SEQ ID NO:2. A dominant negative polypeptide is an inactive variant of a protein, which, by interacting with the cellular machinery, displaces an active protein from its interaction with the cellular machinery or competes with the active protein, thereby reducing the effect of the active protein. For example, a dominant negative receptor which binds a ligand but does not transmit a signal in response to binding of the ligand can reduce the biological effect of expression of the ligand. Likewise, a dominant negative catalytically-inactive kinase which interacts normally with target proteins but does not phosphorylate the target proteins can reduce phosphorylation of the target proteins in response to a cellular signal. Similarly, a dominant negative transcription factor which binds to a promoter site in the control region of a gene but does not increase gene transcription can reduce the effect of a normal transcription factor by occupying promoter binding sites without increasing transcription.

The end result of the expression of a dominant negative polypeptide in a cell is a reduction in function of active proteins. One of ordinary skill in the art can assess the potential for a dominant negative variant of a protein, and using standard mutagenesis techniques to create one or more dominant negative variant polypeptides. For example, given the teachings contained herein of a PARG polypeptide, one of ordinary skill in the art can modify the sequence of the PARG polypeptide by site-specific mutagenesis, scanning mutagenesis, partial gene deletion or truncation, and the like. See, e.g., U.S. Patent No. 5,580,723 and Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989.

The skilled artisan then can test the population of mutagenized polypeptides for diminution in a selected activity (e.g., PARG GAP activity) and for retention of a desired activity (e.g., PARG binding to PTPL1). Other similar methods for creating and testing dominant negative variants of

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a protein will be apparent to one of ordinary skill in the art.

Dominant negative PARG proteins include variants in which a portion of the PDZ4 domain binding site has been mutated or deleted to reduce or eliminate PARG interaction with PTPL1. Other examples include partial deletion PARG variants which have the GAP domain
5 deleted. Such variants retain the capability to bind PTPL1 but cannot enhance GTPase activity in Rho. A GAP-negative PARG variant does not, therefore, stimulate downstream signal transduction pathways such as the Rho pathway.

The invention also involves agents such as polypeptides which bind to PARG polypeptides and to complexes of PARG polypeptides and their phosphatase binding partners.

10 Such binding agents can be used, for example, in screening assays to detect the presence or absence of PARG polypeptides and complexes of PARG polypeptides and their phosphatase binding partners and in purification protocols to isolate PARG polypeptides and complexes of PARG polypeptides and their phosphatase binding partners. Such agents also can be used to inhibit the native activity of the PARG polypeptides or their phosphatase binding partners, for
15 example, by binding to such polypeptides, or their binding partners or both.

The invention, therefore, embraces peptide binding agents which, for example, can be antibodies or fragments of antibodies having the ability to selectively bind to PARG polypeptides. Antibodies include polyclonal and monoclonal antibodies, prepared according to
20 conventional methodology.

Significantly, as is well-known in the art, only a small portion of an antibody molecule, the paratope, is involved in the binding of the antibody to its epitope (see, in general, Clark, W.R. (1986) The Experimental Foundations of Modern Immunology Wiley & Sons, Inc., New York; Roitt, I. (1991) Essential Immunology, 7th Ed., Blackwell Scientific Publications,
25 Oxford). The pFc' and Fc regions, for example, are effectors of the complement cascade but are not involved in antigen binding. An antibody from which the pFc' region has been enzymatically cleaved, or which has been produced without the pFc' region, designated an F(ab')₂ fragment, retains both of the antigen binding sites of an intact antibody. Similarly, an antibody from which the Fc region has been enzymatically cleaved, or which has been produced without the Fc region,
30 designated an Fab fragment, retains one of the antigen binding sites of an intact antibody molecule. Proceeding further, Fab fragments consist of a covalently bound antibody light chain and a portion of the antibody heavy chain denoted Fd. The Fd fragments are the major

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determinant of antibody specificity (a single Fd fragment may be associated with up to ten different light chains without altering antibody specificity) and Fd fragments retain epitope-binding ability in isolation.

Within the antigen-binding portion of an antibody, as is well-known in the art, there are
5 complementarity determining regions (CDRs), which directly interact with the epitope of the antigen, and framework regions (FRs), which maintain the tertiary structure of the paratope (see, in general, Clark, 1986; Roitt, 1991). In both the heavy chain Fd fragment and the light chain of IgG immunoglobulins, there are four framework regions (FR1 through FR4) separated respectively by three complementarity determining regions (CDR1 through CDR3). The CDRs,
10 and in particular the CDR3 regions, and more particularly the heavy chain CDR3, are largely responsible for antibody specificity.

It is now well-established in the art that the non-CDR regions of a mammalian antibody may be replaced with similar regions of conspecific or heterospecific antibodies while retaining the epitopic specificity of the original antibody. This is most clearly manifested in the
15 development and use of "humanized" antibodies in which non-human CDRs are covalently joined to human FR and/or Fc/pFc' regions to produce a functional antibody. Thus, for example, PCT International Publication Number WO 92/04381 teaches the production and use of humanized murine RSV antibodies in which at least a portion of the murine FR regions have been replaced by FR regions of human origin. Such antibodies, including fragments of intact
20 antibodies with antigen-binding ability, are often referred to as "chimeric" antibodies.

Thus, as will be apparent to one of ordinary skill in the art, the present invention also provides for F(ab')₂, Fab, Fv and Fd fragments; chimeric antibodies in which the Fc and/or FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; chimeric F(ab')₂ fragment antibodies in which the FR and/or
25 CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; chimeric Fab fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; and chimeric Fd fragment antibodies in which the FR and/or CDR1 and/or CDR2 regions have been replaced by homologous human or non-human sequences. The present
30 invention also includes so-called single chain antibodies.

Thus, the invention involves polypeptides of numerous size and type that bind specifically to PARG polypeptides, and complexes of both PARG polypeptides and their

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phosphatase binding partners. These polypeptides may be derived also from sources other than antibody technology. For example, such polypeptide binding agents can be provided by degenerate peptide libraries which can be readily prepared in solution, in immobilized form or as phage display libraries. Combinatorial libraries also can be synthesized of peptides containing one or more amino acids. Libraries further can be synthesized of peptoids and non-peptide synthetic moieties.

Phage display can be particularly effective in identifying binding peptides useful according to the invention. Briefly, one prepares a phage library (using e.g. m13, fd, or lambda phage), displaying inserts from 4 to about 80 amino acid residues using conventional procedures. The inserts may represent, for example, a completely degenerate or biased array. One then can select phage-bearing inserts which bind to the PARG polypeptide. This process can be repeated through several cycles of reselection of phage that bind to the PARG polypeptide. Repeated rounds lead to enrichment of phage bearing particular sequences. DNA sequence analysis can be conducted to identify the sequences of the expressed polypeptides. The minimal linear portion of the sequence that binds to the PARG polypeptide can be determined. One can repeat the procedure using a biased library containing inserts containing part or all of the minimal linear portion plus one or more additional degenerate residues upstream or downstream thereof. Yeast two-hybrid screening methods also may be used to identify polypeptides that bind to the PARG polypeptides. Thus, the PARG polypeptides of the invention, or a fragment thereof, can be used to screen peptide libraries, including phage display libraries, to identify and select peptide binding partners of the PARG polypeptides of the invention. Such molecules can be used, as described, for screening assays, for purification protocols, for interfering directly with the functioning of PARG and for other purposes that will be apparent to those of ordinary skill in the art.

A PARG polypeptide, or a fragment which contains the C-terminal PDZ4 domain binding site, also can be used to isolate their native binding partners, including, e.g., the PTPL1 phosphatase that complexes with PARG. Isolation of phosphatases may be performed according to well-known methods. For example, isolated PARG polypeptides can be attached to a substrate, and then a solution suspected of containing the phosphatase may be applied to the substrate. If the phosphatase binding partner for PARG polypeptides is present in the solution, then it will bind to the substrate-bound PARG polypeptide. The phosphatase then may be isolated. Other proteins which are binding partners for PARG, such as other proteins which

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contain PDZ4 domains may be isolated by similar methods without undue experimentation. Similarly, other proteins which bind PARG (e.g. Rho) can be isolated from biological samples and/or extracts by such methods.

Isolation of the PARG protein enables the skilled artisan to use the protein for isolation of molecules which bind to it. For example, isolated PARG can be used to isolate PTPL1 and other proteins which contain PDZ4 domains. The PARG or PDZ binding fragment can be immobilized on chromatographic media, such as polystyrene beads, or a filter, and the immobilized protein can be used to isolate proteins containing a PDZ4 domain from biological samples with no more than routine experimentation according to art-standard procedures for affinity chromatography. Such procedures are described in greater detail below.

It will also be recognized that the invention embraces the use of the PARG cDNA sequences in expression vectors, as well as to transfect host cells and cell lines, be these prokaryotic (e.g., *E. coli*), or eukaryotic (e.g., CHO cells, COS cells, yeast expression systems and recombinant baculovirus expression in insect cells). Especially useful are mammalian cells such as mouse, hamster, pig, goat, primate, etc. They may be of a wide variety of tissue types, and include primary cells and cell lines. Specific examples include dendritic cells, U293 cells, peripheral blood leukocytes, bone marrow stem cells and embryonic stem cells. The expression vectors require that the pertinent sequence, i.e., those nucleic acids described *supra*, be operably linked to a promoter.

When administered, the therapeutic compositions of the present invention are administered in pharmaceutically acceptable preparations. Such preparations may routinely contain pharmaceutically acceptable concentrations of salt, buffering agents, preservatives, compatible carriers, supplementary immune potentiating agents such as adjuvants and cytokines and optionally other therapeutic agents.

The therapeutics of the invention can be administered by any conventional route, including injection or by gradual infusion over time. The administration may, for example, be oral, intravenous, intraperitoneal, intramuscular, intracavity, subcutaneous, or transdermal. When antibodies are used therapeutically, a preferred route of administration is by pulmonary aerosol. Techniques for preparing aerosol delivery systems containing antibodies are well known to those of skill in the art. Generally, such systems should utilize components which will not significantly impair the biological properties of the antibodies, such as the paratope binding capacity (see, for example, Sciarra and Cutie, "Aerosols," in Remington's Pharmaceutical

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Sciences, 18th edition, 1990, pp 1694-1712; incorporated by reference). Those of skill in the art can readily determine the various parameters and conditions for producing antibody aerosols without resort to undue experimentation. When using antisense preparations of the invention, slow intravenous administration is preferred.

5 Preparations for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Aqueous carriers include water, alcoholic/aqueous solutions, emulsions or suspensions, including saline and buffered media. Parenteral vehicles include sodium chloride solution,
10 Ringer's dextrose, dextrose and sodium chloride, lactated Ringer's or fixed oils. Intravenous vehicles include fluid and nutrient replenishers, electrolyte replenishers (such as those based on Ringer's dextrose), and the like. Preservatives and other additives may also be present such as, for example, antimicrobials, anti-oxidants, chelating agents, and inert gases and the like.

The preparations of the invention are administered in effective amounts. An effective
15 amount is that amount of a pharmaceutical preparation that alone, or together with further doses, produces the desired response. In the case of treating cancer, the desired response is inhibiting the progression of the cancer. This may involve only slowing the progression of the disease temporarily, although more preferably, it involves halting the progression of the disease permanently. This can be monitored by routine methods or can be monitored according to
20 diagnostic methods of the invention discussed herein. Other therapeutic uses of PARG include the modulation of actin reorganization, and modulation of mast cell secretory granule release to treat allergic responses.

The invention also contemplates gene therapy. The procedure for performing *ex vivo* gene therapy is outlined in U.S. Patent 5,399,346 and in exhibits submitted in the file history of
25 that patent, all of which are publicly available documents. In general, it involves introduction *in vitro* of a functional copy of a gene into a cell(s) of a subject which contains a defective copy of the gene, and returning the genetically engineered cell(s) to the subject. The functional copy of the gene is under operable control of regulatory elements which permit expression of the gene in the genetically engineered cell(s). Numerous transfection and transduction techniques as well as
30 appropriate expression vectors are well known to those of ordinary skill in the art, some of which are described in PCT application WO95/00654. *In vivo* gene therapy using vectors such as adenovirus, retroviruses, herpes virus, and targeted liposomes also is contemplated according to

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the invention.

The invention further provides efficient methods of identifying pharmacological agents or lead compounds for agents active at the level of a PARG or PARG fragment modulatable cellular function. In particular, such functions include Rho signal transduction and formation of a PTPL1-PARG protein complex. Generally, the screening methods involve assaying for compounds which interfere with a PARG activity such as PARG-PTPL1 binding, etc. Such methods are adaptable to automated, high throughput screening of compounds. The target therapeutic indications for pharmacological agents detected by the screening methods are limited only in that the target cellular function be subject to modulation by alteration of the formation of a complex comprising a PARG polypeptide or fragment thereof and one or more natural PARG intracellular binding targets, such as PTPL1 or other protein including a PDZ 4 domain. Target indications include cellular processes modulated by Rho signal transduction following receptor-ligand binding and PTPL1-mediated phosphorylation.

A wide variety of assays for pharmacological agents are provided, including, labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays, cell-based assays such as two- or three-hybrid screens, expression assays, etc. For example, three-hybrid screens are used to rapidly examine the effect of transfected nucleic acids on the intracellular binding of PARG or PARG fragments to specific intracellular targets. The transfected nucleic acids can encode, for example, combinatorial peptide libraries or antisense molecules. Convenient reagents for such assays, e.g., GAL4 fusion proteins, are known in the art. An exemplary cell-based assay involves transfecting a cell with a nucleic acid encoding a PTPL1-binding PARG polypeptide (e.g., including a PDZ domain binding site) fused to a GAL4 DNA binding domain and a nucleic acid encoding a PTPL1 PDZ 4 domain fused to a transcription activation domain such as VP16. The cell also contains a reporter gene operably linked to a gene expression regulatory region, such as one or more GAL4 binding sites. Activation of reporter gene transcription occurs when the PARG and PTPL1 PDZ 4 fusion polypeptides bind such that the GAL4 DNA binding domain and the VP16 transcriptional activation domain are brought into proximity to enable transcription of the reporter gene. Agents which modulate a PARG polypeptide mediated cell function are then detected through a change in the expression of reporter gene. Methods for determining changes in the expression of a reporter gene are known in the art.

PARG fragments used in the methods, when not produced by a transfected nucleic acid

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are added to an assay mixture as an isolated polypeptide. PARG polypeptides preferably are produced recombinantly, although such polypeptides may be isolated from biological extracts. Recombinantly produced PARG polypeptides include chimeric proteins comprising a fusion of a PARG protein with another polypeptide, e.g., a polypeptide capable of providing or enhancing protein-protein binding, sequence specific nucleic acid binding (such as GAL4), enhancing stability of the PARG polypeptide under assay conditions, or providing a detectable moiety, such as green fluorescent protein. A polypeptide fused to a PARG polypeptide or fragment may also provide means of readily detecting the fusion protein, e.g., by immunological recognition or by fluorescent labeling.

The assay mixture is comprised of a natural intracellular PARG binding target such as a Rho protein, PTPL1 protein or fragment thereof capable of binding to PARG. While natural PARG binding targets may be used, it is frequently preferred to use portions (e.g., peptides or nucleic acid fragments) or analogs (i.e., agents which mimic the PARG binding properties of the natural binding target for purposes of the assay) of the PARG binding target so long as the portion or analog provides binding affinity and avidity to the PARG fragment measurable in the assay.

The assay mixture also comprises a candidate pharmacological agent. Typically, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a different response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration of agent or at a concentration of agent below the limits of assay detection. Candidate agents encompass numerous chemical classes, although typically they are organic compounds. Preferably, the candidate pharmacological agents are small organic compounds, i.e., those having a molecular weight of more than 50 yet less than about 2500, preferably less than about 1000 and, more preferably, less than about 500.

Candidate agents comprise functional chemical groups necessary for structural interactions with polypeptides and/or nucleic acids, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups and more preferably at least three of the functional chemical groups. The candidate agents can comprise cyclic carbon or heterocyclic structure and/or aromatic or polyaromatic structures substituted with one or more of the above-identified functional groups. Candidate agents also can be biomolecules such as peptides, saccharides, fatty acids, sterols, isoprenoids, purines, pyrimidines, derivatives or structural analogs of the above, or combinations thereof and the like. Where the agent is a

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nucleic acid, the agent typically is a DNA or RNA molecule, although modified nucleic acids as defined herein are also contemplated.

Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and
5 directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides, synthetic organic combinatorial libraries, phage display libraries of random peptides, and the like. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available or readily produced. Additionally, natural and synthetically produced libraries and compounds can be readily be
10 modified through conventional chemical, physical, and biochemical means. Further, known pharmacological agents may be subjected to directed or random chemical modifications such as acylation, alkylation, esterification, amidification, etc. to produce structural analogs of the agents.

A variety of other reagents also can be included in the mixture. These include reagents
15 such as salts, buffers, neutral proteins (e.g., albumin), detergents, etc. which may be used to facilitate optimal protein-protein and/or protein-nucleic acid binding. Such a reagent may also reduce non-specific or background interactions of the reaction components. Other reagents that improve the efficiency of the assay such as protease, inhibitors, nuclease inhibitors, antimicrobial agents, and the like may also be used.

The mixture of the foregoing assay materials is incubated under conditions whereby, but
20 for the presence of the candidate pharmacological agent, the PARG polypeptide specifically binds the cellular binding target, a portion thereof or analog thereof. The order of addition of components, incubation temperature, time of incubation, and other perimeters of the assay may be readily determined. Such experimentation merely involves optimization of the assay
25 parameters, not the fundamental composition of the assay. Incubation temperatures typically are between 4°C and 40°C. Incubation times preferably are minimized to facilitate rapid, high throughput screening, and typically are between 0.1 and 10 hours.

After incubation, the presence or absence of specific binding between the PARG
polypeptide and one or more binding targets is detected by any convenient method available to
30 the user. For cell free binding type assays, a separation step is often used to separate bound from unbound components. The separation step may be accomplished in a variety of ways. Conveniently, at least one of the components is immobilized on a solid substrate, from which the

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unbound components may be easily separated. The solid substrate can be made of a wide variety of materials and in a wide variety of shapes, e.g., microtiter plate, microbead, dipstick, resin particle, etc. The substrate preferably is chosen to maximum signal to noise ratios, primarily to minimize background binding, as well as for ease of separation and cost.

5 Separation may be effected for example, by removing a bead or dipstick from a reservoir, emptying or diluting a reservoir such as a microtiter plate well, rinsing a bead, particle, chromatographic column or filter with a wash solution or solvent. The separation step preferably includes multiple rinses or washes. For example, when the solid substrate is a microtiter plate, the wells may be washed several times with a washing solution, which typically includes those
10 components of the incubation mixture that do not participate in specific bindings such as salts, buffer, detergent, non-specific protein, etc. Where the solid substrate is a magnetic bead, the beads may be washed one or more times with a washing solution and isolated using a magnet.

Detection may be effected in any convenient way for cell-based assays such as two- or three-hybrid screens. The transcript resulting from a reporter gene transcription assay of PARG
15 polypeptide binding to a target molecule typically encodes a directly or indirectly detectable product, e.g., β -galactosidase activity, luciferase activity, and the like. For cell free binding assays, one of the components usually comprises, or is coupled to, a detectable label. A wide variety of labels can be used, such as those that provide direct detection (e.g., radioactivity, luminescence, optical or electron density, etc). or indirect detection (e.g., epitope tag such as the
20 FLAG epitope, enzyme tag such as horseshoe peroxidase, etc.). The label may be bound to a PARG binding partner, or incorporated into the structure of the binding partner.

A variety of methods may be used to detect the label, depending on the nature of the label and other assay components. For example, the label may be detected while bound to the solid substrate or subsequent to separation from the solid substrate. Labels may be directly detected
25 through optical or electron density, radioactive emissions, nonradiative energy transfers, etc. or indirectly detected with antibody conjugates, streptavidin-biotin conjugates, etc. Methods for detecting the labels are well known in the art.

The invention provides PARG-specific binding agents, methods of identifying and making such agents, and their use in diagnosis, therapy and pharmaceutical development. For
30 example, PARG-specific pharmacological agents are useful in a variety of diagnostic and therapeutic applications, especially where disease or disease prognosis is associated with improper utilization of a pathway involving PARG, e.g., Rho activation, PTPL1-PARG complex

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formation, etc. Novel PARG-specific binding agents include PARG-specific antibodies and other natural intracellular binding agents identified with assays such as two hybrid screens, and non-natural intracellular binding agents identified in screens of chemical libraries and the like.

In general, the specificity of PARG binding to a binding agent is shown by binding
5 equilibrium constants. Targets which are capable of selectively binding a PARG polypeptide preferably have binding equilibrium constants of at least about 10^7 M^{-1} , more preferably at least about 10^8 M^{-1} , and most preferably at least about 10^9 M^{-1} . The wide variety of cell based and cell free assays may be used to demonstrate PARG-specific binding. Cell based assays include one, two and three hybrid screens, assays in which PARG-mediated transcription is inhibited or
10 increased, etc. Cell free assays include PARG-protein binding assays, immunoassays, etc. Other assays useful for screening agents which bind PARG polypeptides include fluorescence resonance energy transfer (FRET), and electrophoretic mobility shift analysis (EMSA).

Various techniques may be employed for introducing nucleic acids of the invention into cells, depending on whether the nucleic acids are introduced *in vitro* or *in vivo* in a host. Such
15 techniques include transfection of nucleic acid- CaPO_4 precipitates, transfection of nucleic acids associated with DEAE, transfection with a retrovirus including the nucleic acid of interest, liposome mediated transfection, and the like. For certain uses, it is preferred to target the nucleic acid to particular cells. In such instances, a vehicle used for delivering a nucleic acid of the invention into a cell (e.g., a retrovirus, or other virus; a liposome) can have a targeting molecule
20 attached thereto. For example, a molecule such as an antibody specific for a surface membrane protein on the target cell or a ligand for a receptor on the target cell can be bound to or incorporated within the nucleic acid delivery vehicle. For example, where liposomes are employed to deliver the nucleic acids of the invention, proteins which bind to a surface membrane protein associated with endocytosis may be incorporated into the liposome
25 formulation for targeting and/or to facilitate uptake. Such proteins include capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half life, and the like. Polymeric delivery systems also have been used successfully to deliver nucleic acids into cells, as is known by those skilled in the art. Such systems even permit oral
30 delivery of nucleic acids.

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Examples

Example 1: Production of PDZ Fusion Proteins

To identify proteins that bind to the PDZ domains of PTPL1, regions of PTPL1 cDNA corresponding to the various PDZ domains were produced by polymerase chain reaction and subcloned into the GST fusion protein expression vector pGEX1 λ T (Pharmacia): GST-PDZ 1, amino acid residues 1066-1166 of PTPL1; GST-PDZ 2-3, residues 1340-1579; GST-PDZ 3, residues 1469-1579; GST-PDZ 4, residues 1762-1864; GST-PDZ 4-5, residues 1762-1960 and GST-PDZ 5, residues 1856-1960 (Figure 1A). Domains and motifs indicated in Figure 1A are: L, leucine zipper motif; Band 4.1, a domain of 300 amino acid residues with homology to the Band 4.1 superfamily; P, PDZ domain; PTP, protein tyrosine phosphatase catalytic domain; GST, glutathione S-transferase. The different expression vector constructs were transformed into *E. coli*. Glutathione S-transferase (GST) fusion proteins were produced and purified as described by Ridley and Hall (*Cell* 70: 389-399, 1992) and then subjected to sodium dodecyl sulfate (SDS)-gel electrophoresis. Figure 1B shows that pure preparations of fusion proteins with expected sizes were obtained.

Example 2: Identification of Proteins Which Bind to PDZ4

PC-3 cells were obtained from American Type Culture Collection (Rockville, MD) and cultured as described (Saras *et al.*, 1994). Metabolic labeling of PC-3 cells was performed for 4 h in methionine- and cysteine-free MCDB 104 medium (Gibco/Life Technologies, Gaithersburg, MD) with 150 Ci/ml of 35 S-methionine and 35 S-cysteine (*in vivo* labeling mix; Amersham, Arlington Heights, IL). After labeling, the cells were solubilized in buffer containing 20 mM Tris-HCl, pH 7.4, 150 mM NaCl, 10 mM EDTA, 0.5% Triton X-100, 0.5% deoxycholate, 1 mM dithiothreitol, 1.5% Trasylol (Bayer, Germany) and 1 mM phenylmethylsulfonyl fluoride (Sigma, St. Louis, MO). After 15 min on ice, cell debris was removed by centrifugation. Samples (1 ml) were then incubated for 1.5 h at 4°C with 10 μ g of GST-PDZ fusion proteins bound to glutathione-Sepharose 4B beads (Pharmacia). The beads were pelleted and washed four times with solubilization buffer. The protein complexes were eluted by boiling for 5 min in SDS-sample buffer (100 mM Tris-HCl, pH 8.8, 0.01 % bromophenol blue, 36% glycerol, 4% SDS, 10 mM dithiothreitol) and analyzed by SDS-gel electrophoresis using 5-12 % polyacrylamide gels (Blobel and Dobberstein, *J. Cell Biol.* 67: 835-851, 1975). The gel was fixed, incubated with Amplify (Amersham) for 20 min, dried and subjected to fluorography. A

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component of 150 kDa that bound to the fusion proteins GST-PDZ 4 and GST-PDZ-4-5 could be observed (Figure 2); this component did not bind to GST fusion proteins containing PDZ domains 1, 2, 3 or 5 only, thus indicating that the 150 kDa component interacts specifically with PDZ 4 of PTPL1.

5

Example 3: Purification of 150kDa Protein which binds to PDZ4

In order to characterize the 150 kDa component further, it was purified from PC-3 cells. Briefly, immobilized fusion protein GST-PDZ 4 was incubated with cell lysate from 1750 cm² of confluent PC-3 cells solubilized as described above. Samples (20 ml) were incubated for 1.5 h at 10 4°C with 200 µg of GST-PDZ 4 fusion protein bound to glutathione-Sepharose 4B beads. The beads were washed and the bound proteins were eluted and subjected to SDS-gel electrophoresis as described above.

After staining of the gel with Coomassie Brilliant Blue, the band that contained the 150 kDa component was excised and subjected to in-gel digestion using modified trypsin or 15 EndoLysC protease. The band containing the 150 kDa component was transferred to Eppendorf tubes and subjected to in-gel digestion (Hellman *et al.*, *Anal. Biochem.* 224: 451-455, 1995). In brief, the gel piece was washed with 0.2 M ammonium bicarbonate (for digestion with trypsin) or 0.5 M Tris-HCl pH 9.2 (for digestion with EndoLysC protease) and 50 % acetonitrile, then dried completely. During rehydration, 0.5 µg of modified trypsin, sequence grade (Promega, Madison, 20 WI) or 0.5 µg of EndoLysC (WAKO Chemicals, Richmond, VA) was added and 0.2 M ammonium bicarbonate (for trypsin) or 0.1 M Tris-HCl pH 9.2 (for EndoLysC) was added in aliquots until the gel piece was immersed. After overnight incubation at 30°C, the supernatant was saved and combined with two further extractions from the gel piece. Generated peptides were isolated by reversed phase liquid chromatography using the SMART System (Pharmacia 25 Biotech, Uppsala, Sweden). Peptides were sequenced on an Applied Biosystems (Foster City, CA) model 470A or 476A, following the manufacturers instructions.

Sequences were obtained from 10 peptides, and searches in different databases showed that none of these sequences were found in any known gene or protein, but the human Expressed Sequence Tags (ESTs) with GenBank accession numbers T32345, Z28937 and Z28520 (SEQ ID 30 NOs:3, 4, 5), contained cDNA sequences corresponding to three of the obtained peptides. Oligonucleotides corresponding to the nucleotide sequences of the ESTs were designed and used as probes for Northern blots and screening of cDNA libraries.

Example 4: cDNA Cloning of PARG

The EST-derived oligonucleotides described above were used to screen different human cDNA libraries. Briefly, complementary and overlapping oligonucleotides corresponding to nucleotides 2-41 and 68-29 of an EST with the GenBank accession number Z28520 (SEQ ID NO:5) were made using a DNA synthesizer and labeled by a fill-in method (Sambrook *et al.*, 1989) using the Klenow fragment of DNA polymerase I (Amersham) and α -³²P-dCTP (3000Ci/mmol, Amersham). A λ gt11 human skeletal muscle cDNA library (HL5002b; Clontech, Palo Alto, CA) was screened as described (Saras *et al.*, 1994), using the ³²P-labeled oligonucleotides as a probe. A positive clone was isolated, subcloned into pBluescript SK (Stratagene, La Jolla, CA) and thereafter sequenced.

Nucleotide sequencing revealed that the clone had a total length of 5237 bp with an open reading frame of 3783 bp, coding for a protein of 1261 amino acid residues. The open reading frame is flanked by a 5' untranslated sequence of 183 bp that contains an in frame stop codon at positions 166-168, and a 3' untranslated sequence of 1270 bp that has a poly(A) tail. The calculated molecular mass of the translated product is 142 kDa and the protein was, for reasons described below, denoted PARG. The amino acid sequence of PARG (SEQ ID NO:2) is shown in Figure 3A; the nucleotide sequence (SEQ ID NO:1) has been deposited in the EMBL database.

Example 5: Structure of the PARG Protein

The amino acid sequence of PARG contained all peptide sequences obtained previously (Figure 3A). In the deduced amino acid sequence of PARG no transmembrane domain or signal sequence for secretion were found, indicating that PARG is likely an intracellular protein. Three regions with homologies to other proteins could be identified: A GAP domain with similarity (23-33 % amino acid sequence identity) to proteins of the RhoGAP family (Lamarche and Hall, 1994) is found at amino acid residues 666-853, a cysteine-rich region at amino acid residues 613-652 has homology to a regulatory, phorbol ester-, diacylglycerol- and Zn²⁺- binding domain of members of the protein kinase C (PKC) family (Newton, 1995), and a region at amino acid residues 193-509 has homology (27 % identity) to the gene product of the *C. elegans* gene ZK669.1 a (EMBL accession number Z37093). Figure 3B shows an alignment of the latter homology region, denoted ZPH region (for ZK669.1a-PARG homology). The alignment was done using the Clustal method (Higgins and Sharp, CABIOS 5: 151-153, 1989), with some

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manual adjustment. Identical amino acid residues are boxed. Like PARG, the gene product of ZK669.1 contains in addition to the ZPH region, a cysteine-rich domain and a GAP domain (Figure 3C). Domains and motifs indicated in Figure 3C are: ZPH, ZK669.1a-PARG Homology region; C, cysteine-rich domain; GAP, RhoGAP domain.

5

Example 6: Expression of PARG mRNA

Northern blot analysis was performed to determine expression of the PARG mRNA. A Northern blot filter with mRNA from different human tissues was purchased from Clontech. Each lane contained 2 μ g of polyadenylated RNA from the indicated tissues. The filter was
10 hybridized with the 32 P-labeled oligonucleotide probe described above, at 42°C overnight in a hybridization solution containing 50% formamide, 5 x SSC (1x SSC is 15 mM sodium citrate and 150 mM sodium chloride), 2 x Denhardt's solution, 0.5% SDS, 50 mM sodium phosphate, pH 6.9, and 0.1 mg/ml salmon sperm DNA. The filter was washed two times in 0.5 x SSC, 0.1% SDS at 55°C for 15 min. After washing, the filter was exposed to Amersham Hyperfilm MP.

15

Northern blot analysis of mRNA from various human tissues showed that a single PARG transcript of 5.5 kb was found in all screened tissues (Figure 4). The expression of PARG mRNA was high in skeletal muscle and heart and moderate in placenta, liver and pancreas. Low expression was observed in brain, lung and kidney. The size of the transcript suggested that the cDNA clone obtained was close to full length.

20

Example 7: GAP activity of PARG

In order to determine the GAP activity of PARG on proteins of the Rho family, the GAP domain of PARG was produced as a GST fusion protein in *E. coli* (Figure 5A). Briefly, a DNA fragment coding for the GAP domain, i.e., amino acid residues 658-898, of PARG was produced
25 by polymerase chain reaction and subcloned into pGEX1 λ T and referred to as GST-GAP. pGEX2T-based expression vectors containing RhoA, Rac1 and Cdc42 (G25K isoform) cDNAs were obtained from Dr. A. Hall (MRC Laboratory for Molecular Cell Biology and Department of Biochemistry, University College London, UK). These different expression vector constructs were transformed into *E. coli*. The GST fusion proteins were produced and purified essentially
30 as described above in Example 1. Recombinant Rho, Rac and Cdc42 proteins were subjected to thrombin cleavage (Ridley and Hall, 1992).

Recombinant Rho, Rac and Cdc42 were preloaded with γ - 32 P-GTP and incubated for

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various time periods in the presence of the GST-GAP fusion protein or, as control, GST protein. Thereafter, the radioactivity bound to the GTPase was determined as a measurement of the GTP hydrolysis activity. Briefly, 200 nM aliquots of recombinant Rho, Rac and Cdc42 were incubated at 30°C with 10 μ Ci γ -³²P-GTP in 20 mM Tris-HCl, pH 7.5, 25 mM NaCl, 4 mM EDTA, 0.1 mM dithiothreitol, and the nucleotide exchange was stopped after 10 min by the addition of 17 mM MgCl₂. Proteins (100 nM GST, 1 nM or 20 nM of GST-GAP fusion protein) were added to the reaction mixture and aliquots of 5 μ l were withdrawn and collected on nitrocellulose filters (HA, Millipore, Bedford, MA) at 3 min intervals. The filters were washed with cold buffer (50 mM Tris-HCl pH 7.5, 50 mM NaCl, 5 mM MgCl₂), dried and subjected to scintillation counting. The amount of protein-bound radioactivity is expressed as the percentage of the total input.

The results show that the GAP domain of PARG, at the concentration of 1 nM, had a strong GAP activity on Rho (Figure 5B). At this concentration, no GAP activity on Rac or Cdc42 was detected (Figure 5C and 5D). However, at a concentration of 20 nM, the GST-GAP fusion protein was also active on Rac and Cdc42 (Figure 5C and 5D). Thus, the results indicated that PARG has a functional GAP domain which, *in vitro*, is active on Rho, Rac and Cdc42, but with a clear preference for Rho. It is likely, therefore, that Rho is the physiological target of PARG. The name PARG is consequently derived from PTPL1 Associated RhoGAP.

Example 8: PDZ4 Binds to the C-terminal portion of PARG

It has been shown that PDZ domains interact with the C-terminal ends of short peptides and that a valine residue at the absolute C-terminal end is important for binding (Kim *et al.*, 1995; Kornau *et al.*, 1995; Saras *et al.*, in preparation). Since PARG was identified through a specific interaction with PDZ 4 of PTPL1, and since it has a valine residue at the C-terminal end, we found it likely that the interaction is mediated via PDZ 4 and the C-terminal tail of PARG. To verify this possibility, peptides corresponding to the last 4, 5 or 6 C-terminal amino acid residues of PARG (PQFV, IPQFV and EIPQFV; SEQ ID Nos:7, 9 and 11) were synthesized in an Applied Biosystems 430A Peptide Synthesizer using t-butoxycarbonyl chemistry and purified by reversed phase high performance liquid chromatography. The peptides were coupled to Affigel 15 beads (Bio-Rad, Richmond, CA) via their N-terminal ends following the manufacturers instructions and incubated with GST-PDZ fusion proteins (50 nM) at 4°C for 2 h in binding buffer (20 mM Tris-HCl, pH 7.4, 150 mM NaCl, 10 mM EDTA, 0.5% Triton X-100,

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0.5% deoxycholate, 1 mM dithiothreitol). The beads were washed four times in binding buffer and bound fusion proteins were eluted by boiling for 5 min in SDS-sample buffer and subjected to SDS-gel electrophoresis using 11 % polyacrylamide gels. After electrophoresis, the proteins were transferred to nitrocellulose membranes (Hybond C Extra; Amersham) and the membranes were incubated with α -GST antiserum (rabbit antiserum raised against recombinant GST expressed in bacteria). Bound antibodies were visualized by using enhanced chemiluminescence (ECL, Amersham), according to the manufacturer's instructions.

As shown in Figure 6, the fusion proteins GST-PDZ 4 and GST-PDZ 4-5, but not GST fusion proteins containing PDZ 1, PDZ 2, PDZ 3 or PDZ 5 only, bound to the peptide corresponding to the last four amino acid residues of PARG. Similar results were obtained by using the longer peptides, indicating that a maximum of four amino acid residues at the C-terminal end of PARG is enough for a strong and specific interaction with PDZ 4 of PTPL1.

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

All references disclosed herein are incorporated by reference in their entirety.

A Sequence Listing is presented below and is followed by what is claimed.

- 40 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT:

(A) NAME: LUDWIG INSTITUTE FOR CANCER RESEARCH

(B) STREET: 1345 AVENUE OF THE AMERICAS

(C) CITY: NEW YORK

(D) STATE: NEW YORK

10 (E) COUNTRY: UNITED STATES OF AMERICA

(F) POSTAL CODE: 10105

(ii) TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH
INTERACTS WITH PTPL1

15

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.

20 (B) STREET: 600 ATLANTIC AVENUE

(C) CITY: BOSTON

(D) STATE: MASSACHUSETTS

(E) COUNTRY: UNITED STATES OF AMERICA

(F) POSTAL CODE: 02210

25

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

35 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/805,583

(B) FILING DATE: 25-FEB-1997

40

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Van Amsterdam, John R.

(B) REGISTRATION NUMBER: 40,212

(C) REFERENCE/DOCKET NUMBER: L0461/7007WO

45

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 617-720-3500

(B) TELEFAX: 617-720-2441

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 5238 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- 15 (A) NAME/KEY: CDS
 (B) LOCATION: 184..3966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

20 GCTGTGGCTG CGGCTGCGGC TGCGGCTGAG ATTTGGCCGG GCGTCCGCAG GCCGTGGGGG 60
 ATGGGGGCAG CGAGCTCCAG CCCTCGGCGG TGGCGGCGGC CGTAGGTGTG GGGCGGGCGT 120
 CCGCGTCCGG CACGCGAGAT GGAGCGCCGT GGATTTTCAGT TTTTCTGACT GTTACATGAA 180
 25 AGG ATG ATT GCT CAC AAA CAG AAA AAG ACA AAG AAA AAA CGT GCT TGG 228
 Met Ile Ala His Lys Gln Lys Lys Thr Lys Lys Lys Arg Ala Trp
 1 5 10 15
 30 GCA TCA GGT CAA CTC TCT ACT GAT ATT ACA ACT TCT GAA ATG GGG CTC 276
 Ala Ser Gly Gln Leu Ser Thr Asp Ile Thr Thr Ser Glu Met Gly Leu
 20 25 30
 AAG TCC TTA AGT TCC AAC TCT ATT TTT GAT CCG GAT TAC ATC AAG GAG 324
 35 Lys Ser Leu Ser Ser Asn Ser Ile Phe Asp Pro Asp Tyr Ile Lys Glu
 35 40 45
 TTG GTG AAT GAT ATC AGG AAG TTC TCC CAC ATC TTA CTA TAT TTG AAA 372
 Leu Val Asn Asp Ile Arg Lys Phe Ser His Ile Leu Leu Tyr Leu Lys
 40 50 55 60
 GAA GCC ATA TTT TCA GAC TGT TTT AAA GAA GTT ATT CAT ATA CGT CTA 420
 Glu Ala Ile Phe Ser Asp Cys Phe Lys Glu Val Ile His Ile Arg Leu
 65 70 75
 45 GAG GAA CTG CTC CGT GTT TTA AAG TCT ATA ATG AAT AAA CAT CAG AAC 468
 Glu Glu Leu Leu Arg Val Leu Lys Ser Ile Met Asn Lys His Gln Asn
 80 85 90 95

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	CTC AAT TCT GTT GAT CTT CAA AAT GCT GCA GAA ATG CTC ACT GCA AAA	516
	Leu Asn Ser Val Asp Leu Gln Asn Ala Ala Glu Met Leu Thr Ala Lys	
	100 105 110	
5	GTG AAA GCT GTG AAC TTC ACA GAA GTT AAT GAA GAA AAC AAA AAC GAT	564
	Val Lys Ala Val Asn Phe Thr Glu Val Asn Glu Glu Asn Lys Asn Asp	
	115 120 125	
10	CTC TTC CAG GAA GTG TTT TCT TCT ATT GAA ACT TTG GCA TTT ACC TTT	612
	Leu Phe Gln Glu Val Phe Ser Ser Ile Glu Thr Leu Ala Phe Thr Phe	
	130 135 140	
15	GGA AAT ATC CTT ACA AAC TTC CTT ATG GGA GAT GTA GGC AAT GAT TCA	660
	Gly Asn Ile Leu Thr Asn Phe Leu Met Gly Asp Val Gly Asn Asp Ser	
	145 150 155	
20	TTC TTG CGA CTG CCT GTT TCT CGA GAA ACT AAG TCG TTT GAA AAT GTT	708
	Phe Leu Arg Leu Pro Val Ser Arg Glu Thr Lys Ser Phe Glu Asn Val	
	160 165 170 175	
25	TCT GTG GAA TCA GTG GAC TCA TCC AGT GAA AAA GGA AAT TTT TCC CCT	756
	Ser Val Glu Ser Val Asp Ser Ser Ser Glu Lys Gly Asn Phe Ser Pro	
	180 185 190	
30	TTA GAA CTA GAC AAC GTG CTG TTA AAG AAC ACT GAC TCT ATC GAG CTG	804
	Leu Glu Leu Asp Asn Val Leu Leu Lys Asn Thr Asp Ser Ile Glu Leu	
	195 200 205	
35	GCT TTG TCA TAT GCT AAA ACT TGG TCA AAA TAT ACT AAG AAC ATA GTT	852
	Ala Leu Ser Tyr Ala Lys Thr Trp Ser Lys Tyr Thr Lys Asn Ile Val	
	210 215 220	
40	TCA TGG GTT GAA AAA AAG CTT AAC TTG GAA TTG GAG TCC ACT AGA AAT	900
	Ser Trp Val Glu Lys Lys Leu Asn Leu Glu Leu Glu Ser Thr Arg Asn	
	225 230 235	
45	ATG GTC AAG TTG GCA GAG GCA ACT AGA ACT AAC ATT GGA ATT CAG GAG	948
	Met Val Lys Leu Ala Glu Ala Thr Arg Thr Asn Ile Gly Ile Gln Glu	
	240 245 250 255	
50	TTC ATG CCA CTG CAG TCT CTG TTT ACT AAT GCT CTT CTT AAT GAT ATA	996
	Phe Met Pro Leu Gln Ser Leu Phe Thr Asn Ala Leu Leu Asn Asp Ile	
	260 265 270	
55	GAA AGC AGT CAC CTT TTA CAA CAA ACA ATT GCA GCT CTC CAG GCT AAC	1044
	Glu Ser Ser His Leu Leu Gln Gln Thr Ile Ala Ala Leu Gln Ala Asn	
	275 280 285	

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	AAA TTT GTG CAG CCT CTA CTT GGA AGG AAA AAT GAA ATG GAA AAA CAA	1092
	Lys Phe Val Gln Pro Leu Leu Gly Arg Lys Asn Glu Met Glu Lys Gln	
	290 295 300	
5	AGG AAA GAA ATA AAA GAG CTT TGG AAA CAG GAG CAA AAT AAA ATG CTT	1140
	Arg Lys Glu Ile Lys Glu Leu Trp Lys Gln Glu Gln Asn Lys Met Leu	
	305 310 315	
10	GAA GCA GAG AAT GCT CTC AAA AAG GCA AAA TTA TTA TGC ATG CAA CGT	1188
	Glu Ala Glu Asn Ala Leu Lys Lys Ala Lys Leu Leu Cys Met Gln Arg	
	320 325 330 335	
15	CAA GAT GAA TAT GAG AAA GCA AAG TCT TCC ATG TTT CGT GCA GAA GAG	1236
	Gln Asp Glu Tyr Glu Lys Ala Lys Ser Ser Met Phe Arg Ala Glu Glu	
	340 345 350	
20	GAG CAT CTG TCT TCA AGT GGC GGA TTA GCA AAA AAT CTC AAC AAG CAA	1284
	Glu His Leu Ser Ser Ser Gly Gly Leu Ala Lys Asn Leu Asn Lys Gln	
	355 360 365	
25	CTA GAA AAA AAG CGA AGG TTG GAA GAG GAG GCT CTC CAA AAA GTA GAA	1332
	Leu Glu Lys Lys Arg Arg Leu Glu Glu Glu Ala Leu Gln Lys Val Glu	
	370 375 380	
30	GAA GCA GAT GAA CTT TAC AAA GTT TGT GTG ACA AAT GTT GAA GAA AGA	1380
	Glu Ala Asp Glu Leu Tyr Lys Val Cys Val Thr Asn Val Glu Glu Arg	
	385 390 395	
35	AGA AAT GAT GTA GAA AAT ACC AAA AGA GAA ATT TTA GCA CAA CTC CGG	1428
	Arg Asn Asp Val Glu Asn Thr Lys Arg Glu Ile Leu Ala Gln Leu Arg	
	400 405 410 415	
40	ACA CTT GTT TTC CAG TGT GAT CTT ACC CTT AAA GCG GTA ACA GTT AAC	1476
	Thr Leu Val Phe Gln Cys Asp Leu Thr Leu Lys Ala Val Thr Val Asn	
	420 425 430	
45	CTC TTC CAC ATG CAG CAT CTG CAG GCT GCT TCC CTT GCA GAC AGA TTA	1524
	Leu Phe His Met Gln His Leu Gln Ala Ala Ser Leu Ala Asp Arg Leu	
	435 440 445	
50	CAG TCT CTC TGT GGT AGT GCC AAA CTC TAT GAC CCA GGC CAA GAG TAC	1572
	Gln Ser Leu Cys Gly Ser Ala Lys Leu Tyr Asp Pro Gly Gln Glu Tyr	
	450 455 460	
55	AGT GAA TTT GTC AAG GCC ACA AAT TCA ACT GAA GAA GAA AAA GTT GAT	1620
	Ser Glu Phe Val Lys Ala Thr Asn Ser Thr Glu Glu Glu Lys Val Asp	
	465 470 475	

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	GGA AAT GTA AAT AAA CAT TTA AAT AGT TCC CAA CCT TCA GGA TTT GGA	1668
	Gly Asn Val Asn Lys His Leu Asn Ser Ser Gln Pro Ser Gly Phe Gly	
	480 485 490 495	
5	CCT GCC AAC TCT TTA GAG GAT GTT GTA CGC CTT CCT GAC AGT TCT AAT	1716
	Pro Ala Asn Ser Leu Glu Asp Val Val Arg Leu Pro Asp Ser Ser Asn	
	500 505 510	
10	AAA ATT GAA GAG GAC AGA TGC TCT AAC AGT GCA GAT ATA ACA GGT CCT	1764
	Lys Ile Glu Glu Asp Arg Cys Ser Asn Ser Ala Asp Ile Thr Gly Pro	
	515 520 525	
15	TCC TTT ATA AGA TCA TGG ACA TTT GGG ATG TTT AGT GAT TCT GAG AGC	1812
	Ser Phe Ile Arg Ser Trp Thr Phe Gly Met Phe Ser Asp Ser Glu Ser	
	530 535 540	
20	ACT GGA GGG AGC AGC GAA TCT AGA TCT CTG GAT TCA GAA TCT ATA AGT	1860
	Thr Gly Gly Ser Ser Glu Ser Arg Ser Leu Asp Ser Glu Ser Ile Ser	
	545 550 555	
25	CCA GGA GAC TTT CAT CGA AAA CTT CCA CGA ACA CCA TCC AGT GGA ACT	1908
	Pro Gly Asp Phe His Arg Lys Leu Pro Arg Thr Pro Ser Ser Gly Thr	
	560 565 570 575	
30	ATG TCC TCT GCA GAT GAT CTA GAT GAA AGA GAG CCA CCT TCC CCT TCA	1956
	Met Ser Ser Ala Asp Asp Leu Asp Glu Arg Glu Pro Pro Ser Pro Ser	
	580 585 590	
35	GAA ACT GGA CCC AAT TCC CTT GGA ACA TTT AAG AAA ACA TTG ATG TCA	2004
	Glu Thr Gly Pro Asn Ser Leu Gly Thr Phe Lys Lys Thr Leu Met Ser	
	595 600 605	
40	AAG GCA GCT CTC ACA CAC AAG TTT CGC AAA TTG AGA TCC CCC ACG AAA	2052
	Lys Ala Ala Leu Thr His Lys Phe Arg Lys Leu Arg Ser Pro Thr Lys	
	610 615 620	
45	TGT AGG GAT TGT GAA GGC ATT GTA GTG TTC CAA GGT GTT GAA TGT GAA	2100
	Cys Arg Asp Cys Glu Gly Ile Val Val Phe Gln Gly Val Glu Cys Glu	
	625 630 635	
50	GAG TGT CTC CTT GTT TGT CAT CGA AAG TGT TTG GAA AAT TTA GTC ATT	2148
	Glu Cys Leu Leu Val Cys His Arg Lys Cys Leu Glu Asn Leu Val Ile	
	640 645 650 655	
55	ATT TGT GGT CAT CAG AAA CTT CCA GGA AAA ATA CAC TTA TTT GGA GCA	2196
	Ile Cys Gly His Gln Lys Leu Pro Gly Lys Ile His Leu Phe Gly Ala	
	660 665 670	

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	GAA TTC ACA CTA GTT GCA AAA AAG GAA CCA GAT GGT ATC CCT TTT ATA	2244
	Glu Phe Thr Leu Val Ala Lys Lys Glu Pro Asp Gly Ile Pro Phe Ile	
	675 680 685	
5	CTC AAA ATA TGT GCC TCA GAG ATT GAA AAT AGA GCT TTG TGT CTA CAG	2292
	Leu Lys Ile Cys Ala Ser Glu Ile Glu Asn Arg Ala Leu Cys Leu Gln	
	690 695 700	
10	GGA ATT TAT CGT GTG TGT GGA AAC AAA ATA AAA ACT GAA AAA TTG TGT	2340
	Gly Ile Tyr Arg Val Cys Gly Asn Lys Ile Lys Thr Glu Lys Leu Cys	
	705 710 715	
	CTA GCT TTG GAA AAT GGT ATG CAC TTG GTA GAT ATT TCA GAA TTT AGT	2388
	Leu Ala Leu Glu Asn Gly Met His Leu Val Asp Ile Ser Glu Phe Ser	
15	720 725 730 735	
	TCA CAT GAT ATC TGT GAC GTC TTG AAA TTA TAC CTT CGG CAG CTC CCA	2436
	Ser His Asp Ile Cys Asp Val Leu Lys Leu Tyr Leu Arg Gln Leu Pro	
	740 745 750	
20	GAA CCA TTT ATT TTA TTT CGA TTG TAC AAG GAA TTT ATA GAC CTT GCA	2484
	Glu Pro Phe Ile Leu Phe Arg Leu Tyr Lys Glu Phe Ile Asp Leu Ala	
	755 760 765	
25	AAA GAG ATC CAA CAT GTA AAT GAA GAA CAA GAG ACA AAA AAG AAT AGT	2532
	Lys Glu Ile Gln His Val Asn Glu Glu Gln Glu Thr Lys Lys Asn Ser	
	770 775 780	
30	CTT GAA GAC AAA AAA TGG CCA AAT ATG TGT ATA GAA ATA AAC CGA ATT	2580
	Leu Glu Asp Lys Lys Trp Pro Asn Met Cys Ile Glu Ile Asn Arg Ile	
	785 790 795	
	CTT CTA AAA AGC AAA GAC CTT CTA AGA CAA TTG CCA GCA TCA AAT TTT	2628
	Leu Leu Lys Ser Lys Asp Leu Leu Arg Gln Leu Pro Ala Ser Asn Phe	
35	800 805 810 815	
	AAC AGT CTT CAT TTC CTT ATA GTA CAT CTA AAG CGG GTA GTA GAT CAT	2676
	Asn Ser Leu His Phe Leu Ile Val His Leu Lys Arg Val Val Asp His	
	820 825 830	
40	GCA GAA GAA AAC AAG ATG AAC TCC AAA AAC TTG GGG GTG ATA TTT GGA	2724
	Ala Glu Glu Asn Lys Met Asn Ser Lys Asn Leu Gly Val Ile Phe Gly	
	835 840 845	
45	CCA AGT CTC ATT AGG CCA AGG CCA CAA ACT GCT CCT ATC ACC ATC TCC	2772
	Pro Ser Leu Ile Arg Pro Arg Pro Gln Thr Ala Pro Ile Thr Ile Ser	
	850 855 860	

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	TCC	CTT	GCA	GAG	TAT	TCA	AAT	CAA	GCA	CGC	TTG	GTA	GAG	TTT	CTC	ATT	2820
	Ser	Leu	Ala	Glu	Tyr	Ser	Asn	Gln	Ala	Arg	Leu	Val	Glu	Phe	Leu	Ile	
	865					870					875						
5	ACT	TAC	TCA	CAG	AAG	ATC	TTC	GAT	GGG	TCC	CTA	CAA	CCA	CAA	GAT	GTT	2868
	Thr	Tyr	Ser	Gln	Lys	Ile	Phe	Asp	Gly	Ser	Leu	Gln	Pro	Gln	Asp	Val	
	880					885					890					895	
	ATG	TGT	AGC	ATA	GGT	GTT	GTT	GAT	CAA	GGC	TGT	TTT	CCA	AAG	CCT	CTG	2916
10	Met	Cys	Ser	Ile	Gly	Val	Val	Asp	Gln	Gly	Cys	Phe	Pro	Lys	Pro	Leu	
					900					905						910	
	TTA	TCA	CCA	GAA	GAA	AGA	GAC	ATT	GAA	CGT	TCC	ATG	AAG	TCA	CTA	TTT	2964
15	Leu	Ser	Pro	Glu	Glu	Arg	Asp	Ile	Glu	Arg	Ser	Met	Lys	Ser	Leu	Phe	
				915					920					925			
	TTT	TCT	TCA	AAG	GAA	GAT	ATC	CAT	ACT	TCA	GAG	AGT	GAA	AGC	AAA	ATT	3012
	Phe	Ser	Ser	Lys	Glu	Asp	Ile	His	Thr	Ser	Glu	Ser	Glu	Ser	Lys	Ile	
				930				935					940				
20	TTT	GAA	CGA	GCT	ACA	TCA	TTT	GAG	GAA	TCA	GAA	CGC	AAG	CAA	AAT	GCG	3060
	Phe	Glu	Arg	Ala	Thr	Ser	Phe	Glu	Glu	Ser	Glu	Arg	Lys	Gln	Asn	Ala	
		945					950					955					
25	TTA	GGA	AAA	TGT	GAT	GCA	TGT	CTC	AGT	GAC	AAA	GCA	CAG	TTG	CTT	CTA	3108
	Leu	Gly	Lys	Cys	Asp	Ala	Cys	Leu	Ser	Asp	Lys	Ala	Gln	Leu	Leu	Leu	
	960					965					970					975	
	GAC	CAA	GAG	GCT	GAA	TCA	GCA	TCC	CAA	AAG	ATA	GAA	GAT	GGT	AAA	GCC	3156
30	Asp	Gln	Glu	Ala	Glu	Ser	Ala	Ser	Gln	Lys	Ile	Glu	Asp	Gly	Lys	Ala	
					980					985					990		
	CCT	AAG	CCA	CTT	TCT	CTG	AAA	TCT	GAT	AGG	TCA	ACA	AAC	AAT	GTG	GAG	3204
35	Pro	Lys	Pro	Leu	Ser	Leu	Lys	Ser	Asp	Arg	Ser	Thr	Asn	Asn	Val	Glu	
				995					1000					1005			
	AGG	CAT	ACT	CCA	AGG	ACC	AAG	ATT	AGA	CCT	GTA	AGT	TTG	CCT	GTA	GAT	3252
	Arg	His	Thr	Pro	Arg	Thr	Lys	Ile	Arg	Pro	Val	Ser	Leu	Pro	Val	Asp	
				1010				1015					1020				
40	AGA	CTA	CTT	CTT	GCA	AGT	CCT	CCT	AAT	GAG	AGA	AAT	GGC	AGA	AAT	ATG	3300
	Arg	Leu	Leu	Leu	Ala	Ser	Pro	Pro	Asn	Glu	Arg	Asn	Gly	Arg	Asn	Met	
		1025					1030					1035					
45	GGA	AAT	GTA	AAT	TTA	GAC	AAG	TTT	TGC	AAG	AAT	CCT	GCC	TTT	GAA	GGA	3348
	Gly	Asn	Val	Asn	Leu	Asp	Lys	Phe	Cys	Lys	Asn	Pro	Ala	Phe	Glu	Gly	
	1040					1045					1050				1055		

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	GTT AAT AGA AAA GAC GCT GCT ACT ACT GTT TGT TCC AAA TTT AAT GGC	3396
	Val Asn Arg Lys Asp Ala Ala Thr Thr Val Cys Ser Lys Phe Asn Gly	
	1060 1065 1070	
5	TTT GAC CAG CAA ACT CTA CAG AAA ATT CAG GAC AAA CAG TAT GAA CAA	3444
	Phe Asp Gln Gln Thr Leu Gln Lys Ile Gln Asp Lys Gln Tyr Glu Gln	
	1075 1080 1085	
	AAC AGC CTA ACT GCC AAG ACT ACA ATG ATC ATG CCC AGT GCA CTC CAG	3492
10	Asn Ser Leu Thr Ala Lys Thr Thr Met Ile Met Pro Ser Ala Leu Gln	
	1090 1095 1100	
	GAA AAA GGA GTG ACA ACA AGC CTC CAG ATT AGT GGG GAC CAT TCT ATC	3540
15	Glu Lys Gly Val Thr Thr Ser Leu Gln Ile Ser Gly Asp His Ser Ile	
	1105 1110 1115	
	AAT GCC ACT CAA CCC AGT AAG CCA TAT GCA GAG CCA GTC AGG TCA GTG	3588
	Asn Ala Thr Gln Pro Ser Lys Pro Tyr Ala Glu Pro Val Arg Ser Val	
	1120 1125 1130 1135	
20	AGA GAG GCA TCT GAG AGA CCG TCT TCA GAT TCC TAC CCT CTC GCT CCT	3636
	Arg Glu Ala Ser Glu Arg Arg Ser Ser Asp Ser Tyr Pro Leu Ala Pro	
	1140 1145 1150	
25	GTC AGA GCA CCC AGA ACA CTG CAG CCT CAA CAT TGG ACA ACA TTT TAT	3684
	Val Arg Ala Pro Arg Thr Leu Gln Pro Gln His Trp Thr Thr Phe Tyr	
	1155 1160 1165	
	AAA CCA CAT GCT CCC ATC ATC AGT ATC AGG GGG AAT GAG GAG AAG CCA	3732
30	Lys Pro His Ala Pro Ile Ile Ser Ile Arg Gly Asn Glu Glu Lys Pro	
	1170 1175 1180	
	GCT TCA CCC TCA GCA GCA TGC CCT CCT GGC ACA GAT CAC GAT CCC CAC	3780
35	Ala Ser Pro Ser Ala Ala Cys Pro Pro Gly Thr Asp His Asp Pro His	
	1185 1190 1195	
	GGT CTC GTG GTG AAG TCA ATG CCA GAC CCA GAC AAA GCA TCA GCT TGT	3828
	Gly Leu Val Val Lys Ser Met Pro Asp Pro Asp Lys Ala Ser Ala Cys	
	1200 1205 1210 1215	
40	CCT GGG CAA GCA ACT GGT CAA CCT AAA GAA GAC TCT GAG GAG CTT GGC	3876
	Pro Gly Gln Ala Thr Gly Gln Pro Lys Glu Asp Ser Glu Glu Leu Gly	
	1220 1225 1230	
45	TTG CCT GAT GTG AAT CCA ATG TGT CAG AGA CCA AGG CTA AAA CGA ATG	3924
	Leu Pro Asp Val Asn Pro Met Cys Gln Arg Pro Arg Leu Lys Arg Met	
	1235 1240 1245	

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	CAA CAG TTT GAA GAC CTC GAA GAT GAA ATT CCA CAA TTT GTG	3966
	Gln Gln Phe Glu Asp Leu Glu Asp Glu Ile Pro Gln Phe Val	
	1250 1255 1260	
5	TAGGGATGTC AAATTTTCAGG GTTTTTTTTGT TGTGTGTGTG TTATTTTGTG GTATTGTGCT	4026
	TGTTTTGTGA AAGAATGTTT TGACAGGGCC CCTTTTGTAT AGGACTGCCA AATCATGGGT	4086
	TTTGCCTTTT GTTGTGTGTAT TTATCCTCTG TTGGTAATAC TGAATGGTAG AATGTTTTGA	4146
10	TAGGGTCACA TTTGTGCCTC ACTGGAATTA TCCTTAAATT CTGTATTTTT AAAGTTGTGA	4206
	ATAAGATAGG TGGATTGTA TTTTTTAAAG TTCAGTTGAC TTTCCCCACC AAATGGTCCA	4266
15	TTTGAATGCA TCCCTAATAT ATGATATAGT CTCAACTAAT AGGTGCAATT TGGGAAAATC	4326
	AGGTTTATTT TTTGGAGTGG AACTGTTATA AGTGCTTATT TATAAAAGGA ATGTTTCTGA	4386
	ATGCAAGTGC CTAAAAAGAT CTTTGTGTGT ATGCATATGT TTTGTCACAC AATTTATAGT	4446
20	GCATCTTTCA CCATTGTGC TTTTTTAAGA TAGTATGTAA GCTCTTATTT TTCAATTGGC	4506
	AATTCAGTTA ATTTTTAAAT GTTTACATAA TGGCCAGAAG GCTTGCAAAT CTGTATTTAA	4566
25	TTGCATTTTA ATTAATTGCC AGTTTTTACA TGTAGTAGTC AGTTGTACAA AGAAAATGCA	4626
	CTTAAACCTG TTTCTAAATT ATATATTCAG TTATATTATA TTTGGCTTTA GATGGTTTTA	4686
	ATACATTTGA TAGTTTTTCA CCCCTTGGCT TTATTTTATA TAAACTTTTG TTTTTCAGCA	4746
30	GTTCTGAACT TTTTAGTATT TTATAAATGG TCCAAAAAAT GCCTGTTTCA GAAGTTTTTG	4806
	AATTCAGTGC ATTCCTCTT GATTGTCTG GGTTAAAACC ATTCCTTTTG TATGAAATGT	4866
35	TTTGACTTAG GAATCATTTT ATGTACTTGT TCTACCTGGA TTGTCAACAA CTGAAAGTAC	4926
	ATATTTTCATC CAAATCAAGC TAAAATTTAT TTAAGTTGAT TCTGAGAGTA CAGGTCAGTA	4986
	AGCCTCATTA TTTGGAATTT GAGAGAAGTA TAGGTGATCG GATCTGTTTC ATTTATAAAA	5046
40	GGTCCAGTTT TTAGGACTAG TACATTCCTG TTATTTTCTG GGTTTTATCA TTTTGCCTAA	5106
	AATAGGATAT AAAAGGGACA AAAAATAAGT AGACTGTTTT TATGTGTGAA TTATATTTCT	5166
45	ACTAAATGTT TTTGTATGAC TGTGTTATAC TTGATAATAT ATATATATAT ATATAAAAAA	5226
	AAAAAAAAAA AA	5238

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1261 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ile Ala His Lys Gln Lys Lys Thr Lys Lys Lys Arg Ala Trp Ala
 1 5 10 15

Ser Gly Gln Leu Ser Thr Asp Ile Thr Thr Ser Glu Met Gly Leu Lys
 20 25 30

Ser Leu Ser Ser Asn Ser Ile Phe Asp Pro Asp Tyr Ile Lys Glu Leu
 35 40 45

Val Asn Asp Ile Arg Lys Phe Ser His Ile Leu Leu Tyr Leu Lys Glu
 50 55 60

Ala Ile Phe Ser Asp Cys Phe Lys Glu Val Ile His Ile Arg Leu Glu
 65 70 75 80

Glu Leu Leu Arg Val Leu Lys Ser Ile Met Asn Lys His Gln Asn Leu
 85 90 95

Asn Ser Val Asp Leu Gln Asn Ala Ala Glu Met Leu Thr Ala Lys Val
 100 105 110

Lys Ala Val Asn Phe Thr Glu Val Asn Glu Glu Asn Lys Asn Asp Leu
 115 120 125

Phe Gln Glu Val Phe Ser Ser Ile Glu Thr Leu Ala Phe Thr Phe Gly
 130 135 140

Asn Ile Leu Thr Asn Phe Leu Met Gly Asp Val Gly Asn Asp Ser Phe
 145 150 155 160

Leu Arg Leu Pro Val Ser Arg Glu Thr Lys Ser Phe Glu Asn Val Ser
 165 170 175

Val Glu Ser Val Asp Ser Ser Ser Glu Lys Gly Asn Phe Ser Pro Leu
 180 185 190

Glu Leu Asp Asn Val Leu Leu Lys Asn Thr Asp Ser Ile Glu Leu Ala

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	195	200	205
	Leu Ser Tyr Ala Lys Thr Trp Ser Lys Tyr Thr Lys Asn Ile Val Ser		
	210	215	220
5	Trp Val Glu Lys Lys Leu Asn Leu Glu Leu Glu Ser Thr Arg Asn Met		
	225	230	235 240
	Val Lys Leu Ala Glu Ala Thr Arg Thr Asn Ile Gly Ile Gln Glu Phe		
10	245	250	255
	Met Pro Leu Gln Ser Leu Phe Thr Asn Ala Leu Leu Asn Asp Ile Glu		
	260	265	270
15	Ser Ser His Leu Leu Gln Gln Thr Ile Ala Ala Leu Gln Ala Asn Lys		
	275	280	285
	Phe Val Gln Pro Leu Leu Gly Arg Lys Asn Glu Met Glu Lys Gln Arg		
	290	295	300
20	Lys Glu Ile Lys Glu Leu Trp Lys Gln Glu Gln Asn Lys Met Leu Glu		
	305	310	315 320
	Ala Glu Asn Ala Leu Lys Lys Ala Lys Leu Leu Cys Met Gln Arg Gln		
25	325	330	335
	Asp Glu Tyr Glu Lys Ala Lys Ser Ser Met Phe Arg Ala Glu Glu Glu		
	340	345	350
30	His Leu Ser Ser Ser Gly Gly Leu Ala Lys Asn Leu Asn Lys Gln Leu		
	355	360	365
	Glu Lys Lys Arg Arg Leu Glu Glu Glu Ala Leu Gln Lys Val Glu Glu		
	370	375	380
35	Ala Asp Glu Leu Tyr Lys Val Cys Val Thr Asn Val Glu Glu Arg Arg		
	385	390	395 400
	Asn Asp Val Glu Asn Thr Lys Arg Glu Ile Leu Ala Gln Leu Arg Thr		
40	405	410	415
	Leu Val Phe Gln Cys Asp Leu Thr Leu Lys Ala Val Thr Val Asn Leu		
	420	425	430
45	Phe His Met Gln His Leu Gln Ala Ala Ser Leu Ala Asp Arg Leu Gln		
	435	440	445
	Ser Leu Cys Gly Ser Ala Lys Leu Tyr Asp Pro Gly Gln Glu Tyr Ser		

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	450		455		460
	Glu Phe Val Lys Ala Thr Asn Ser Thr Glu Glu Glu Lys Val Asp Gly				
	465		470		475 480
5	Asn Val Asn Lys His Leu Asn Ser Ser Gln Pro Ser Gly Phe Gly Pro				
		485		490	495
10	Ala Asn Ser Leu Glu Asp Val Val Arg Leu Pro Asp Ser Ser Asn Lys				
		500		505	510
	Ile Glu Glu Asp Arg Cys Ser Asn Ser Ala Asp Ile Thr Gly Pro Ser				
		515		520	525
15	Phe Ile Arg Ser Trp Thr Phe Gly Met Phe Ser Asp Ser Glu Ser Thr				
		530		535	540
	Gly Gly Ser Ser Glu Ser Arg Ser Leu Asp Ser Glu Ser Ile Ser Pro				
		545		550	555 560
20	Gly Asp Phe His Arg Lys Leu Pro Arg Thr Pro Ser Ser Gly Thr Met				
		565		570	575
	Ser Ser Ala Asp Asp Leu Asp Glu Arg Glu Pro Pro Ser Pro Ser Glu				
25		580		585	590
	Thr Gly Pro Asn Ser Leu Gly Thr Phe Lys Lys Thr Leu Met Ser Lys				
		595		600	605
30	Ala Ala Leu Thr His Lys Phe Arg Lys Leu Arg Ser Pro Thr Lys Cys				
		610		615	620
	Arg Asp Cys Glu Gly Ile Val Val Phe Gln Gly Val Glu Cys Glu Glu				
		625		630	635 640
35	Cys Leu Leu Val Cys His Arg Lys Cys Leu Glu Asn Leu Val Ile Ile				
		645		650	655
	Cys Gly His Gln Lys Leu Pro Gly Lys Ile His Leu Phe Gly Ala Glu				
40		660		665	670
	Phe Thr Leu Val Ala Lys Lys Glu Pro Asp Gly Ile Pro Phe Ile Leu				
		675		680	685
45	Lys Ile Cys Ala Ser Glu Ile Glu Asn Arg Ala Leu Cys Leu Gln Gly				
		690		695	700
	Ile Tyr Arg Val Cys Gly Asn Lys Ile Lys Thr Glu Lys Leu Cys Leu				

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	705		710		715		720									
	Ala	Leu	Glu	Asn	Gly	Met	His	Leu	Val	Asp	Ile	Ser	Glu	Phe	Ser	Ser
					725					730					735	
5	His	Asp	Ile	Cys	Asp	Val	Leu	Lys	Leu	Tyr	Leu	Arg	Gln	Leu	Pro	Glu
				740					745					750		
	Pro	Phe	Ile	Leu	Phe	Arg	Leu	Tyr	Lys	Glu	Phe	Ile	Asp	Leu	Ala	Lys
10			755					760					765			
	Glu	Ile	Gln	His	Val	Asn	Glu	Glu	Gln	Glu	Thr	Lys	Lys	Asn	Ser	Leu
		770					775					780				
15	Glu	Asp	Lys	Lys	Trp	Pro	Asn	Met	Cys	Ile	Glu	Ile	Asn	Arg	Ile	Leu
	785					790					795					800
	Leu	Lys	Ser	Lys	Asp	Leu	Leu	Arg	Gln	Leu	Pro	Ala	Ser	Asn	Phe	Asn
20				805					810					815		
	Ser	Leu	His	Phe	Leu	Ile	Val	His	Leu	Lys	Arg	Val	Val	Asp	His	Ala
			820						825					830		
	Glu	Glu	Asn	Lys	Met	Asn	Ser	Lys	Asn	Leu	Gly	Val	Ile	Phe	Gly	Pro
25			835					840					845			
	Ser	Leu	Ile	Arg	Pro	Arg	Pro	Gln	Thr	Ala	Pro	Ile	Thr	Ile	Ser	Ser
	850						855					860				
30	Leu	Ala	Glu	Tyr	Ser	Asn	Gln	Ala	Arg	Leu	Val	Glu	Phe	Leu	Ile	Thr
	865					870					875					880
	Tyr	Ser	Gln	Lys	Ile	Phe	Asp	Gly	Ser	Leu	Gln	Pro	Gln	Asp	Val	Met
35				885					890					895		
	Cys	Ser	Ile	Gly	Val	Val	Asp	Gln	Gly	Cys	Phe	Pro	Lys	Pro	Leu	Leu
				900					905					910		
	Ser	Pro	Glu	Glu	Arg	Asp	Ile	Glu	Arg	Ser	Met	Lys	Ser	Leu	Phe	Phe
40			915					920					925			
	Ser	Ser	Lys	Glu	Asp	Ile	His	Thr	Ser	Glu	Ser	Glu	Ser	Lys	Ile	Phe
			930				935					940				
45	Glu	Arg	Ala	Thr	Ser	Phe	Glu	Glu	Ser	Glu	Arg	Lys	Gln	Asn	Ala	Leu
	945					950					955					960
	Gly	Lys	Cys	Asp	Ala	Cys	Leu	Ser	Asp	Lys	Ala	Gln	Leu	Leu	Leu	Asp

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	965	970	975
	Gln Glu Ala Glu Ser Ala Ser Gln Lys Ile Glu Asp Gly Lys Ala Pro		
	980	985	990
5	Lys Pro Leu Ser Leu Lys Ser Asp Arg Ser Thr Asn Asn Val Glu Arg		
	995	1000	1005
	His Thr Pro Arg Thr Lys Ile Arg Pro Val Ser Leu Pro Val Asp Arg		
10	1010	1015	1020
	Leu Leu Leu Ala Ser Pro Pro Asn Glu Arg Asn Gly Arg Asn Met Gly		
	1025	1030	1035 1040
15	Asn Val Asn Leu Asp Lys Phe Cys Lys Asn Pro Ala Phe Glu Gly Val		
	1045	1050	1055
	Asn Arg Lys Asp Ala Ala Thr Thr Val Cys Ser Lys Phe Asn Gly Phe		
	1060	1065	1070
20	Asp Gln Gln Thr Leu Gln Lys Ile Gln Asp Lys Gln Tyr Glu Gln Asn		
	1075	1080	1085
	Ser Leu Thr Ala Lys Thr Thr Met Ile Met Pro Ser Ala Leu Gln Glu		
25	1090	1095	1100
	Lys Gly Val Thr Thr Ser Leu Gln Ile Ser Gly Asp His Ser Ile Asn		
	1105	1110	1115 1120
30	Ala Thr Gln Pro Ser Lys Pro Tyr Ala Glu Pro Val Arg Ser Val Arg		
	1125	1130	1135
	Glu Ala Ser Glu Arg Arg Ser Ser Asp Ser Tyr Pro Leu Ala Pro Val		
	1140	1145	1150
35	Arg Ala Pro Arg Thr Leu Gln Pro Gln His Trp Thr Thr Phe Tyr Lys		
	1155	1160	1165
	Pro His Ala Pro Ile Ile Ser Ile Arg Gly Asn Glu Glu Lys Pro Ala		
40	1170	1175	1180
	Ser Pro Ser Ala Ala Cys Pro Pro Gly Thr Asp His Asp Pro His Gly		
	1185	1190	1195 1200
45	Leu Val Val Lys Ser Met Pro Asp Pro Asp Lys Ala Ser Ala Cys Pro		
	1205	1210	1215
	Gly Gln Ala Thr Gly Gln Pro Lys Glu Asp Ser Glu Glu Leu Gly Leu		

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1220

1225

1230

Pro Asp Val Asn Pro Met Cys Gln Arg Pro Arg Leu Lys Arg Met Gln
 1235 1240 1245

5

Gln Phe Glu Asp Leu Glu Asp Glu Ile Pro Gln Phe Val
 1250 1255 1260

(2) INFORMATION FOR SEQ ID NO:3:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTAATAGAAA AGACGCTGCT ACTACTGTTT GTTCCAAATT TAATGGCTTT GACCAGCAAA 60
 25 CTCTACAGAA AATTCAGGAC AAACAGTATG AACAAAACAG CCTAACTGCC AAGACTACAA 120
 TGATCATGCC CAGTGCACTC CAGGAAAAAG GAGTGACAAC AAGCCTCCAG ATTAGTGGGG 180
 ACCATTCTAT CAATGCCACT NAACCCAGTA AGCCATATGC AGAGCCAGTC AGGTCAGTGA 240
 30 GAGAGGCATC T 251

(2) INFORMATION FOR SEQ ID NO:4:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGTAAGCCA AGCTCCTCAG AGTCTTCTTT AGGTTNACCA GTTGCTTGCC CAGGACAAGC 60

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TGATGCTTTG TCTGGGTCTG GCATTGACTT CACCACGAGA CCGTGGGGAT CGTGATCTGT 120
GCCAGGAGGC ACTGCTGCTG AGGGTGAAGC TGGCTTCTCC TCATTCCCCC TGATACTGAT 180
5 GATGGGAGCA TGTGGTTTAT AAAATGTTGT CCAATGTTGA GGCTGCAGTG TTCTGGGTGC 240
TCTGACAGGA GCGAGA 256

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTTCTGTGA TAGTGCCAAA CTCTATGACC CAGGCCAAGA GTACAGTGAA TTTGTCAAGG 60
25 CCACAAATTC AACTGAAGAA GAAAAAGTTG ATGGAAATGT AAATAAACAT TTAAATAGTT 120
CCCAACCTTC AGGATTTGGN CCTGCCAACT CTTTAGAGGA TGTGTACGC CTCCTGACA 180
GTTCTAATAA AATTGAAGAG GACAGATGCT CTAACAGTGC AGNTATAACA GGTCCCTCCT 240
30 TTATAAGATC ATGGACATTT GGGATGTTTA GTGATTCTGA GAGCACTGGA GGGAGCAG 298

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCACAATTTG TG

12

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Pro Gln Phe Val
1

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATTCCACAAT TTGTG

15

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ile Pro Gln Phe Val

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1

5

(2) INFORMATION FOR SEQ ID NO:10:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAAATTCCAC AATTGTG

18

(2) INFORMATION FOR SEQ ID NO:11:

20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

30

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Glu Ile Pro Gln Phe Val

1

5

35

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2466 amino acids
40 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

45

(iii) HYPOTHETICAL: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

5	Met	His	Val	Ser	Leu	Ala	Glu	Ala	Leu	Glu	Val	Arg	Gly	Gly	Pro	Leu	1	5	10	15
	Gln	Glu	Glu	Glu	Ile	Trp	Ala	Val	Leu	Asn	Gln	Ser	Ala	Glu	Ser	Leu	20	25	30	
10	Gln	Glu	Leu	Phe	Arg	Lys	Val	Ser	Leu	Ala	Asp	Pro	Ala	Ala	Leu	Gly	35	40	45	
	Phe	Ile	Ile	Ser	Pro	Trp	Ser	Leu	Leu	Leu	Leu	Pro	Ser	Gly	Ser	Val	50	55	60	
15	Ser	Phe	Thr	Asp	Glu	Asn	Ile	Ser	Asn	Gln	Asp	Leu	Arg	Ala	Phe	Thr	65	70	75	80
	Ala	Pro	Glu	Val	Leu	Gln	Asn	Gln	Ser	Leu	Thr	Ser	Leu	Ser	Asp	Val	85	90	95	
20	Glu	Lys	Ile	His	Ile	Tyr	Ser	Leu	Gly	Met	Thr	Leu	Tyr	Trp	Gly	Ala	100	105	110	
	Asp	Tyr	Glu	Val	Pro	Gln	Ser	Gln	Pro	Ile	Lys	Leu	Gly	Asp	His	Leu	115	120	125	
25	Asn	Ser	Ile	Leu	Leu	Gly	Met	Cys	Glu	Asp	Val	Ile	Tyr	Ala	Arg	Val	130	135	140	
30	Ser	Val	Arg	Thr	Val	Leu	Asp	Ala	Cys	Ser	Ala	His	Ile	Arg	Asn	Ser	145	150	155	160
	Asn	Cys	Ala	Pro	Ser	Phe	Ser	Tyr	Val	Lys	His	Leu	Val	Lys	Leu	Val	165	170	175	
35	Leu	Gly	Asn	Leu	Ser	Gly	Thr	Asp	Gln	Leu	Ser	Cys	Asn	Ser	Glu	Gln	180	185	190	
40	Lys	Pro	Asp	Arg	Ser	Gln	Ala	Ile	Arg	Asp	Arg	Leu	Arg	Gly	Lys	Gly	195	200	205	
	Leu	Pro	Thr	Gly	Arg	Ser	Ser	Thr	Ser	Asp	Val	Leu	Asp	Ile	Gln	Lys	210	215	220	
45	Pro	Pro	Leu	Ser	His	Gln	Thr	Phe	Leu	Asn	Lys	Gly	Leu	Ser	Lys	Ser	225	230	235	240
	Met	Gly	Phe	Leu	Ser	Ile	Lys	Asp	Thr	Gln	Asp	Glu	Asn	Tyr	Phe	Lys				

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	245	250	255
	Asp Ile Leu Ser Asp Asn Ser Gly Arg Glu Asp Ser Glu Asn Thr Phe		
	260	265	270
5	Ser Pro Tyr Gln Phe Lys Thr Ser Gly Pro Glu Lys Lys Pro Ile Pro		
	275	280	285
10	Gly Ile Asp Val Leu Ser Lys Lys Lys Ile Trp Ala Ser Ser Met Asp		
	290	295	300
	Leu Leu Cys Thr Ala Asp Arg Asp Phe Ser Ser Gly Glu Thr Ala Thr		
	305	310	315
15	Tyr Arg Arg Cys His Pro Glu Ala Val Thr Val Arg Thr Ser Thr Thr		
	325	330	335
	Pro Arg Lys Lys Glu Ala Arg Tyr Ser Asp Gly Ser Ile Ala Leu Asp		
	340	345	350
20	Ile Phe Gly Pro Gln Lys Met Asp Pro Ile Tyr His Thr Arg Glu Leu		
	355	360	365
	Pro Thr Ser Ser Ala Ile Ser Ser Ala Leu Asp Arg Ile Arg Glu Arg		
25	370	375	380
	Gln Lys Lys Leu Gln Val Leu Arg Glu Ala Met Asn Val Glu Glu Pro		
	385	390	395
30	Val Arg Arg Tyr Lys Thr Tyr His Gly Asp Val Phe Ser Thr Ser Ser		
	405	410	415
	Glu Ser Pro Ser Ile Ile Ser Ser Glu Ser Asp Phe Arg Gln Val Arg		
	420	425	430
35	Arg Ser Glu Ala Ser Lys Arg Phe Glu Ser Ser Ser Gly Leu Pro Gly		
	435	440	445
	Val Asp Glu Thr Leu Ser Gln Gly Gln Ser Gln Arg Pro Ser Arg Gln		
40	450	455	460
	Tyr Glu Thr Pro Phe Glu Gly Asn Leu Ile Asn Gln Glu Ile Met Leu		
	465	470	475
45	Lys Arg Gln Glu Glu Glu Leu Met Gln Leu Gln Ala Lys Met Ala Leu		
	485	490	495
	Arg Gln Ser Arg Leu Ser Leu Tyr Pro Gly Asp Thr Ile Lys Ala Ser		

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	500	505	510
	Met Leu Asp Ile Thr Arg Asp	Pro Leu Arg Glu Ile	Ala Leu Glu Thr
	515	520	525
5	Ala Met Thr Gln Arg Lys	Leu Arg Asn Phe Phe Gly	Pro Glu Phe Val
	530	535	540
10	Lys Met Thr Ile Glu Pro Phe	Ile Ser Leu Asp Leu Pro Arg Ser	Ile
	545	550	555 560
	Leu Thr Lys Lys Gly Lys Asn Glu Asp	Asn Arg Arg Lys Val Asn	Ile
	565	570	575
15	Met Leu Leu Asn Gly Gln Arg	Leu Glu Leu Thr Cys Asp Thr Lys Thr	
	580	585	590
	Ile Cys Lys Asp Val Phe Asp	Met Val Val Ala His Ile Gly Leu Val	
	595	600	605
20	Glu His His Leu Phe Ala Leu Ala Thr	Leu Lys Asp Asn Glu Tyr Phe	
	610	615	620
	Phe Val Asp Pro Asp Leu Lys Leu Thr	Lys Val Ala Pro Glu Gly Trp	
25	625	630	635 640
	Lys Glu Glu Pro Lys Lys Lys Thr	Lys Ala Thr Val Asn Phe Thr Leu	
	645	650	655
30	Phe Phe Arg Ile Lys Phe Phe Met	Asp Asp Val Ser Leu Ile Gln His	
	660	665	670
	Thr Leu Thr Cys His Gln Tyr Tyr	Leu Gln Leu Arg Lys Asp Ile Leu	
	675	680	685
35	Glu Glu Arg Met His Cys Asp Asp	Glu Thr Ser Leu Leu Leu Ala Ser	
	690	695	700
	Leu Ala Leu Gln Ala Glu Tyr Gly Asp	Tyr Gln Pro Glu Val His Gly	
40	705	710	715 720
	Val Ser Tyr Phe Arg Met Glu His Tyr	Leu Pro Ala Arg Val Met Glu	
	725	730	735
45	Lys Leu Asp Leu Ser Tyr Ile Lys	Glu Glu Leu Pro Lys Leu His Asn	
	740	745	750
	Thr Tyr Val Gly Ala Ser Glu Lys	Glu Thr Glu Leu Glu Phe Leu Lys	

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	755		760		765
	Val Cys Gln Arg Leu Thr Glu Tyr Gly Val His Phe His Arg Val His				
	770		775		780
5	Pro Glu Lys Lys Ser Gln Thr Gly Ile Leu Leu Gly Val Cys Ser Lys				
	785		790		795 800
	Gly Val Leu Val Phe Glu Val His Asn Gly Val Arg Thr Leu Val Leu				
10		805		810	815
	Arg Phe Pro Trp Arg Glu Thr Lys Lys Ile Ser Phe Ser Lys Lys Lys				
		820		825	830
15	Ile Thr Leu Gln Asn Thr Ser Asp Gly Ile Lys His Gly Phe Gln Thr				
	835		840		845
	Asp Asn Ser Lys Ile Cys Gln Tyr Leu Leu His Leu Cys Ser Tyr Gln				
20	850		855		860
	His Lys Phe Gln Leu Gln Met Arg Ala Arg Gln Ser Asn Gln Asp Ala				
	865		870		875 880
	Gln Asp Ile Glu Arg Ala Ser Phe Arg Ser Leu Asn Leu Gln Ala Glu				
25		885		890	895
	Ser Val Arg Gly Phe Asn Met Gly Arg Ala Ile Ser Thr Gly Ser Leu				
		900		905	910
30	Ala Ser Ser Thr Leu Asn Lys Leu Ala Val Arg Pro Leu Ser Val Gln				
	915		920		925
	Ala Glu Ile Leu Lys Arg Leu Ser Cys Ser Glu Leu Ser Leu Tyr Gln				
35		930		935	940
	Pro Leu Gln Asn Ser Ser Lys Glu Lys Asn Asp Lys Ala Ser Trp Glu				
	945		950		955 960
	Glu Lys Pro Arg Glu Met Ser Lys Ser Tyr His Asp Leu Ser Gln Ala				
40		965		970	975
	Ser Leu Tyr Pro His Arg Lys Asn Val Ile Val Asn Met Glu Pro Pro				
		980		985	990
45	Pro Gln Thr Val Ala Glu Leu Val Gly Lys Pro Ser His Gln Met Ser				
	995		1000		1005
	Arg Ser Asp Ala Glu Ser Leu Ala Gly Val Thr Lys Leu Asn Asn Ser				

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	1010	1015	1020
	Lys Ser Val Ala Ser Leu Asn Arg Ser Pro Glu Arg Arg Lys His Glu		
	1025	1030	1035 1040
5	Ser Asp Ser Ser Ser Ile Glu Asp Pro Gly Gln Ala Tyr Val Leu Asp		
	1045	1050	1055
	Val Leu His Lys Arg Trp Ser Ile Val Ser Ser Pro Glu Arg Glu Ile		
10	1060	1065	1070
	Thr Leu Val Asn Leu Lys Lys Asp Ala Lys Tyr Gly Leu Gly Phe Gln		
	1075	1080	1085
15	Ile Ile Gly Gly Glu Lys Met Gly Arg Leu Asp Leu Gly Ile Phe Ile		
	1090	1095	1100
	Ser Ser Val Ala Pro Gly Gly Pro Ala Asp Phe His Gly Cys Leu Lys		
	1105	1110	1115 1120
20	Pro Gly Asp Arg Leu Ile Ser Val Asn Ser Val Ser Leu Glu Gly Val		
	1125	1130	1135
	Ser His His Ala Ala Ile Glu Ile Leu Gln Asn Ala Pro Glu Asp Val		
25	1140	1145	1150
	Thr Leu Val Ile Ser Gln Pro Lys Glu Lys Ile Ser Lys Val Pro Ser		
	1155	1160	1165
30	Thr Pro Val His Leu Thr Asn Glu Met Lys Asn Tyr Met Lys Lys Ser		
	1170	1175	1180
	Ser Tyr Met Gln Asp Ser Ala Ile Asp Ser Ser Ser Lys Asp His His		
	1185	1190	1195 1200
35	Trp Ser Arg Gly Thr Leu Arg His Ile Ser Glu Asn Ser Phe Gly Pro		
	1205	1210	1215
	Ser Gly Gly Leu Arg Glu Gly Ser Leu Ser Ser Gln Asp Ser Arg Thr		
40	1220	1225	1230
	Glu Ser Ala Ser Leu Ser Gln Ser Gln Val Asn Gly Phe Phe Ala Ser		
	1235	1240	1245
45	His Leu Gly Asp Gln Thr Trp Gln Glu Ser Gln His Gly Ser Pro Ser		
	1250	1255	1260
	Pro Ser Val Ile Ser Lys Ala Thr Glu Lys Glu Thr Phe Thr Asp Ser		

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	1265		1270		1275		1280
	Asn Gln Ser Lys Thr Lys Lys Pro Gly Ile Ser Asp Val Thr Asp Tyr						
			1285		1290		1295
5	Ser Asp Arg Gly Asp Ser Asp Met Asp Glu Ala Thr Tyr Ser Ser Ser						
			1300		1305		1310
	Gln Asp His Gln Thr Pro Lys Gln Glu Ser Ser Ser Ser Val Asn Thr						
10			1315		1320		1325
	Ser Asn Lys Met Asn Phe Lys Thr Phe Ser Ser Ser Pro Pro Lys Pro						
			1330		1335		1340
15	Gly Asp Ile Phe Glu Val Glu Leu Ala Lys Asn Asp Asn Ser Leu Gly						
			1345		1350		1355
							1360
	Ile Ser Val Thr Gly Gly Val Asn Thr Ser Val Arg His Gly Gly Ile						
			1365		1370		1375
20	Tyr Val Lys Ala Val Ile Pro Gln Gly Ala Ala Glu Ser Asp Gly Arg						
			1380		1385		1390
	Ile His Lys Gly Asp Arg Val Leu Ala Val Asn Gly Val Ser Leu Glu						
25			1395		1400		1405
	Gly Ala Thr His Lys Gln Ala Val Glu Thr Leu Arg Asn Thr Gly Gln						
			1410		1415		1420
30	Val Val His Leu Leu Leu Glu Lys Gly Gln Ser Pro Thr Ser Lys Glu						
			1425		1430		1435
							1440
	His Val Pro Val Thr Pro Gln Cys Thr Leu Ser Asp Gln Asn Ala Gln						
			1445		1450		1455
35	Gly Gln Gly Pro Glu Lys Val Lys Lys Thr Thr Gln Val Lys Asp Tyr						
			1460		1465		1470
	Ser Phe Val Thr Glu Glu Asn Thr Phe Glu Val Lys Leu Phe Lys Asn						
40			1475		1480		1485
	Ser Ser Gly Leu Gly Phe Ser Phe Ser Arg Glu Asp Asn Leu Ile Pro						
			1490		1495		1500
45	Glu Gln Ile Asn Ala Ser Ile Val Arg Val Lys Lys Leu Phe Ala Gly						
			1505		1510		1515
							1520
	Gln Pro Ala Ala Glu Ser Gly Lys Ile Asp Val Gly Asp Val Ile Leu						

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	1525	1530	1535
	Lys Val Asn Gly Ala Ser Leu	Lys Gly Leu Ser Gln Gln Glu Val Ile	
	1540	1545	1550
5	Ser Ala Leu Arg Gly Thr Ala Pro Glu Val Phe Leu Leu Leu Cys Arg		
	1555	1560	1565
	Pro Pro Pro Gly Val Leu Pro Glu Ile Asp Thr Ala Leu Leu Thr Pro		
10	1570	1575	1580
	Leu Gln Ser Pro Ala Gln Val Leu Pro Asn Ser Ser Lys Asp Ser Ser		
	1585	1590	1595 1600
15	Gln Pro Ser Cys Val Glu Gln Ser Thr Ser Ser Asp Glu Asn Glu Met		
	1605	1610	1615
	Ser Asp Lys Ser Lys Lys Gln Cys Lys Ser Pro Ser Arg Arg Asp Ser		
	1620	1625	1630
20	Tyr Ser Asp Ser Ser Gly Ser Gly Glu Asp Asp Leu Val Thr Ala Pro		
	1635	1640	1645
	Ala Asn Ile Ser Asn Ser Thr Trp Ser Ser Ala Leu His Gln Thr Leu		
25	1650	1655	1660
	Ser Asn Met Val Ser Gln Ala Gln Ser His His Glu Ala Pro Lys Ser		
	1665	1670	1675 1680
30	Gln Glu Asp Thr Ile Cys Thr Met Phe Tyr Tyr Pro Gln Lys Ile Pro		
	1685	1690	1695
	Asn Lys Pro Glu Phe Glu Asp Ser Asn Pro Ser Pro Leu Pro Pro Asp		
	1700	1705	1710
35	Met Ala Pro Gly Gln Ser Tyr Gln Pro Gln Ser Glu Ser Ala Ser Ser		
	1715	1720	1725
	Ser Ser Met Asp Lys Tyr His Ile His His Ile Ser Glu Pro Thr Arg		
40	1730	1735	1740
	Gln Glu Asn Trp Thr Pro Leu Lys Asn Asp Leu Glu Asn His Leu Glu		
	1745	1750	1755 1760
45	Asp Phe Glu Leu Glu Val Glu Leu Leu Ile Thr Leu Ile Lys Ser Glu		
	1765	1770	1775
	Lys Ala Ser Leu Gly Phe Thr Val Thr Lys Gly Asn Gln Arg Ile Gly		

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	1780	1785	1790
	Cys Tyr Val His Asp Val Ile Gln Asp Pro Ala Lys Ser Asp Gly Arg		
	1795	1800	1805
5	Leu Lys Pro Gly Asp Arg Leu Ile Lys Val Asn Asp Thr Asp Val Thr		
	1810	1815	1820
	Asn Met Thr His Thr Asp Ala Val Asn Leu Leu Arg Ala Ala Ser Lys		
10	1825	1830	1835 1840
	Thr Val Arg Leu Val Ile Gly Arg Val Leu Glu Leu Pro Arg Ile Pro		
	1845	1850	1855
15	Met Leu Pro His Leu Leu Pro Asp Ile Thr Leu Thr Cys Asn Lys Glu		
	1860	1865	1870
	Glu Leu Gly Phe Ser Leu Cys Gly Gly His Asp Ser Leu Tyr Gln Val		
	1875	1880	1885
20	Val Tyr Ile Ser Asp Ile Asn Pro Arg Ser Val Ala Ala Ile Glu Gly		
	1890	1895	1900
	Asn Leu Gln Leu Leu Asp Val Ile His Tyr Val Asn Gly Val Ser Thr		
25	1905	1910	1915 1920
	Gln Gly Met Thr Leu Glu Glu Val Asn Arg Ala Leu Asp Met Ser Leu		
	1925	1930	1935
30	Pro Ser Leu Val Leu Lys Ala Thr Arg Asn Asp Leu Pro Val Val Pro		
	1940	1945	1950
	Ser Ser Lys Arg Ser Ala Val Ser Ala Pro Lys Ser Thr Lys Gly Asn		
	1955	1960	1965
35	Gly Ser Tyr Ser Val Gly Ser Cys Ser Gln Pro Ala Leu Thr Pro Asn		
	1970	1975	1980
	Asp Ser Phe Ser Thr Val Ala Gly Glu Glu Ile Asn Glu Ile Ser Tyr		
40	1985	1990	1995 2000
	Pro Lys Gly Lys Cys Ser Thr Tyr Gln Ile Lys Gly Ser Pro Asn Leu		
	2005	2010	2015
45	Thr Leu Pro Lys Glu Ser Tyr Ile Gln Glu Asp Asp Ile Tyr Asp Asp		
	2020	2025	2030
	Ser Gln Glu Ala Glu Val Ile Gln Ser Leu Leu Asp Val Val Asp Glu		

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	2035	2040	2045
	Glu Ala Gln Asn Leu Leu Asn Glu Asn Asn Ala Ala Gly Tyr Ser Cys		
	2050	2055	2060
5	Gly Pro Gly Thr Leu Lys Met Asn Gly Lys Leu Ser Glu Glu Arg Thr		
	2065	2070	2075 2080
10	Glu Asp Thr Asp Cys Asp Gly Ser Pro Leu Pro Glu Tyr Phe Thr Glu		
	2085	2090	2095
	Ala Thr Lys Met Asn Gly Cys Glu Glu Tyr Cys Glu Glu Lys Val Lys		
	2100	2105	2110
15	Ser Glu Ser Leu Ile Gln Lys Pro Gln Glu Lys Lys Thr Asp Asp Asp		
	2115	2120	2125
	Glu Ile Thr Trp Gly Asn Asp Glu Leu Pro Ile Glu Arg Thr Asn His		
	2130	2135	2140
20	Glu Asp Ser Asp Lys Asp His Ser Phe Leu Thr Asn Asp Glu Leu Ala		
	2145	2150	2155 2160
	Val Leu Pro Val Val Lys Val Leu Pro Ser Gly Lys Tyr Thr Gly Ala		
25	2165	2170	2175
	Asn Leu Lys Ser Val Ile Arg Val Leu Arg Gly Leu Leu Asp Gln Gly		
	2180	2185	2190
30	Ile Pro Ser Lys Glu Leu Glu Asn Leu Gln Glu Leu Lys Pro Leu Asp		
	2195	2200	2205
	Gln Cys Leu Ile Gly Gln Thr Lys Glu Asn Arg Arg Lys Asn Arg Tyr		
	2210	2215	2220
35	Lys Asn Ile Leu Pro Tyr Asp Ala Thr Arg Val Pro Leu Gly Asp Glu		
	2225	2230	2235 2240
	Gly Gly Tyr Ile Asn Ala Ser Phe Ile Lys Ile Pro Val Gly Lys Glu		
40	2245	2250	2255
	Glu Phe Val Tyr Ile Ala Cys Gln Gly Pro Leu Pro Thr Thr Val Gly		
	2260	2265	2270
45	Asp Phe Trp Gln Met Ile Trp Glu Gln Lys Ser Thr Val Ile Ala Met		
	2275	2280	2285
	Met Thr Gln Glu Val Glu Gly Glu Lys Ile Lys Cys Gln Arg Tyr Trp		

- 67 -

	2290	2295	2300
	Pro Asn Ile Leu Gly Lys Thr Thr Met Val Ser Asn Arg Leu Arg Leu		
	2305	2310	2315 2320
5	Ala Leu Val Arg Met Gln Gln Leu Lys Gly Phe Val Val Arg Ala Met		
	2325	2330	2335
	Thr Leu Glu Asp Ile Gln Thr Arg Glu Val Arg His Ile Ser His Leu		
10	2340	2345	2350
	Asn Phe Thr Ala Trp Pro Asp His Asp Thr Pro Ser Gln Pro Asp Asp		
	2355	2360	2365
15	Leu Leu Thr Phe Ile Ser Tyr Met Arg His Ile His Arg Ser Gly Pro		
	2370	2375	2380
	Ile Ile Thr His Cys Ser Ala Gly Ile Gly Arg Ser Gly Thr Leu Ile		
20	2385	2390	2395 2400
	Cys Ile Asp Val Val Leu Gly Leu Ile Ser Gln Asp Leu Asp Phe Asp		
	2405	2410	2415
	Ile Ser Asp Leu Val Arg Cys Met Arg Leu Gln Arg His Gly Met Val		
25	2420	2425	2430
	Gln Thr Glu Asp Gln Tyr Ile Phe Cys Tyr Gln Val Ile Leu Tyr Val		
	2435	2440	2445
30	Leu Thr Arg Leu Gln Ala Glu Glu Glu Gln Lys Gln Gln Pro Gln Leu		
	2450	2455	2460
	Leu Lys		
35	2465		

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

	CTACTGTTTG TTCCAAATTT AATGGCTTTG ACCAGCAAAC TCTACAGAAA ATTCAGGACA	60
5	AACAGTATGA ACAAACAGC CTAAGTCCA AGACTACAAT GATCATGCCC AGTGCACTCC	120
	AGGAAAAAGG AGTGACAACA AGCCTCCAGA TTAGTGGGGA CCATTCTATC AATGCCACTC	180
	AACCCAGTAA GCCATATGCA GAGCCAGTCA GGTCAGTNAG AGAGGCATCT GAGAGACGGT	240
10	CTTCAGATTC CTACCCTCTC G	261

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CLAIMS

1. An isolated nucleic acid molecule selected from the group consisting of
 - (a) nucleic acid molecules which hybridize under stringent conditions to a molecule consisting of the nucleic acid sequence of SEQ ID NO:1 and which codes for a GTPase-
5 activating polypeptide,
 - (b) nucleic acid molecules that differ from the nucleic acid molecules of (a) in codon sequence due to the degeneracy of the genetic code, and
 - (c) complements of (a) and (b).
- 10 2. The isolated nucleic acid molecule of claim 1, wherein the isolated nucleic acid molecule comprises nucleotides 184-3966 of SEQ ID NO:1.
3. The isolated nucleic acid molecule of claim 1, wherein the isolated nucleic acid molecule consists essentially of SEQ ID NO:1.
- 15 4. The isolated nucleic acid molecule of claim 1, wherein the isolated nucleic acid molecule comprises a molecule having a sequence which encodes amino acids 658-898 of SEQ ID NO:2.
5. An isolated nucleic acid molecule selected from the group consisting of (a) a unique
20 fragment of nucleotides 184-3966 of SEQ ID NO:1 between 12 and 3781 nucleotides in length and (b) complements of "(a)", provided that the nucleic acid molecule excludes sequences consisting only of SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5 and SEQ ID NO:13.
6. The isolated nucleic acid molecule of claim 5, wherein the isolated nucleic acid molecule
25 consists of at least 14 contiguous nucleotides.
7. The isolated nucleic acid molecule of claim 5, wherein the isolated nucleic acid molecule consists of at least 15 contiguous nucleotides.
- 30 8. The isolated nucleic acid molecule of claim 5, wherein the isolated nucleic acid molecule consists of at least 16 contiguous nucleotides.

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9. The isolated nucleic acid molecule of claim 5, wherein the isolated nucleic acid molecule consists of at least 17 contiguous nucleotides.

10. The isolated nucleic acid molecule of claim 5, wherein the isolated nucleic acid molecule
5 consists of at least 18 contiguous nucleotides.

11. The isolated nucleic acid molecule of claim 5, wherein the isolated nucleic acid molecule consists of at least 20 contiguous nucleotides.

10 12. The isolated nucleic acid molecule of claim 5, wherein the isolated nucleic acid molecule consists of at least 22 contiguous nucleotides.

13. The isolated nucleic acid molecule of claim 5, wherein the isolated nucleic acid molecule consists of between 12 and 32 contiguous nucleotides.

15

14. An isolated nucleic acid molecule selected from the group consisting of
(a) a molecule having a sequence selected from the group consisting of SEQ ID NO:6,
SEQ ID NO:8 and SEQ ID NO:10;

(b) nucleic acid molecules that differ from the nucleic acid molecules of (a) in codon
20 sequence due to the degeneracy of the genetic code; and
(c) complements of (a) and (b).

15. An expression vector comprising the isolated nucleic acid molecule of claims 1, 2, 3, 4, 5,
6, 7, 8, 9, 10, 11, 12, 13, or 14 operably linked to a promoter.

25

16. A host cell transformed or transfected with the expression vector of claim 15.

17. An isolated polypeptide encoded by the isolated nucleic acid molecule of claim 1, 2
or 4, wherein the polypeptide has GTPase activating activity.

30

18. The isolated polypeptide of claim 17, wherein the isolated polypeptide comprises a
polypeptide having the sequence of amino acids 658-898 of SEQ ID NO:2.

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19. An isolated polypeptide comprising a polypeptide having the sequence of amino acids 613-652 of SEQ ID NO:2, wherein the isolated polypeptide is a cysteine-rich domain.

20. An isolated polypeptide comprising a polypeptide having the sequence of amino acid
5 193-509 of SEQ ID NO:2, wherein the isolated polypeptide is a ZPH domain polypeptide.

21. The isolated polypeptide of any of claims 1, 2, 4, 19, or 20, wherein the isolated polypeptide consists of a functional fragment or variant.

10 22. An isolated polypeptide comprising a polypeptide selected from the group consisting of a polypeptide having the sequence of SEQ ID NO:7, a polypeptide having the sequence of SEQ ID NO:9, and a polypeptide having the sequence of SEQ ID NO:11.

23. The isolated polypeptide of claim 22, wherein the polypeptide consists essentially of a
15 polypeptide selected from the group consisting of a polypeptide having the sequence of SEQ ID NO:7, a polypeptide having the sequence of SEQ ID NO:9, and a polypeptide having the sequence of SEQ ID NO:11.

24. An isolated polypeptide which binds selectively a polypeptide encoded by the isolated
20 nucleic acid molecule of claim 1, 2, 4, or 14, provided that the isolated polypeptide is not PTPL1.

25. The isolated polypeptide of claim 24, wherein the isolated polypeptide binds to a polypeptide comprising the sequence of amino acids 658-898 of SEQ ID NO:2.

25 26. The isolated polypeptide of claim 24, wherein the isolated polypeptide binds to a polypeptide selected from the group consisting of a polypeptide comprising the sequence of SEQ ID NO:7, a polypeptide comprising the sequence of SEQ ID NO:9, and a polypeptide comprising the sequence of SEQ ID NO:11.

30 27. The isolated polypeptide of claim 24, wherein the isolated polypeptide binds to a polypeptide consisting essentially of the sequence of SEQ ID NO:2.

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28. The isolated polypeptide of claim 24, wherein the isolated polypeptide is an antibody fragment selected from the group consisting of a Fab fragment, a F(ab)₂ fragment or a fragment including a CDR3 region selective for a PARG polypeptide.

5 29. An isolated complex of polypeptides comprising:
a polypeptide comprising the amino acid sequence of SEQ ID NO:12 bound to a polypeptide as claimed in claim 1, wherein the complex has phosphatase and GTPase activating activities.

10 30. The isolated complex of polypeptides of claim 29, wherein the polypeptides consist of the polypeptide of SEQ ID NO:12 and the polypeptide of SEQ ID NO:2.

31. A method for reducing Rho family signal transduction in a mammalian cell, comprising administering to the mammalian cell an amount of the isolated polypeptide of claim 17
15 effective to reduce Rho family signal transduction in the mammalian cell.

32. A method for reducing Rho family signal transduction in a mammalian cell, comprising administering to the mammalian cell an amount of the isolated polypeptide complex of claim 29 effective to reduce Rho family signal transduction in the mammalian cell.

20

33. A method for reducing the proliferation of a cancer cell, the proliferation of which is increased by Rho family protein signal transduction, comprising
administering to the cancer cell an amount of a polypeptide comprising a polypeptide encoded by the nucleic acid of SEQ ID NO:1 effective to reduce proliferation of the cancer cell.

25

34. A method of increasing Rho family protein signal transduction in a cell comprising administering to the cell an amount of a dominant-negative variant of the polypeptide of SEQ ID NO:2 effective to increase the Rho family protein signal transduction in the cell.

30 35. The method of claim 34, wherein the dominant negative polypeptide has an inactivated GTPase-activating domain.

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36. The method of claim 35, wherein the inactivated GTPase-activating domain is deleted.

37. The method of claim 35, wherein the inactivated GTPase-activating domain contains at least one inactivating point mutation.

5

38. A method of reducing binding of a protein which includes a PDZ4 domain to a protein which includes a PDZ4 domain binding site in a mammalian cell, comprising
contacting the mammalian cell with an agent which binds to the PDZ4 domain for a time effective to reduce binding of the protein which includes a PDZ4 domain to the protein which
10 includes a PDZ4 domain binding site.

39. The method of claim 38, wherein the agent is a peptide comprising [at its carboxyl terminus] the amino acid sequence of SEQ ID NO:7, or conservative amino acid substitutions thereof excepting the terminal valine.

15

40. The method of claim 39, wherein the agent is a peptide selected from the group consisting of a peptide having the amino acid sequence of SEQ ID NO:7, a peptide having the amino acid sequence of SEQ ID NO:9 and a peptide having the amino acid sequence of SEQ ID
NO:11.

20

41. The method of claim 38, wherein the agent is an antibody which binds to the PDZ4 domain.

42. The method of claim 41, wherein the antibody is a monoclonal antibody.

25

43. A method of modulating mast cell secretion in a subject, comprising:
administering to the subject in need of such treatment an amount of a modulator of
PARG GTPase activating activity effective to modulate mast cell secretion.

30 44. A composition comprising:
the polypeptide of claim 17, and
a pharmaceutically acceptable carrier.

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45. A composition comprising:
the polypeptide complex of claim 29, and
a pharmaceutically acceptable carrier.

5 46. A composition comprising:
the agent of claim 39, and
a pharmaceutically acceptable carrier.

47. A method for decreasing PARG GTPase activity in a subject comprising
10 administering to a subject in need of such treatment an agent that selectively binds to an
isolated nucleic acid molecule of claim 1 or an expression product thereof, in an amount effective
to decrease PARG GTPase activity in the subject.

48. The method of claim 47, wherein the agent is an antisense nucleic acid.
15

49. The method of claim 47, wherein the agent is a polypeptide.

50. A method for identifying lead compounds for a pharmacological agent useful in the
diagnosis or treatment of disease associated with PARG GTPase activating activity, comprising
20 forming a mixture comprising a PARG polypeptide or unique fragment thereof
containing a PARG GTPase activating domain, a protein containing a GTPase specifically
activatable by the PARG GTPase activating domain, and a candidate pharmacological agent,
incubating the mixture under conditions which, in the absence of the candidate
pharmacological agent, permit a first amount of specific activation of the GTPase by the PARG
25 GTPase activating domain, and
detecting a test amount of the specific activation of the GTPase by the PARG GTPase
activating domain, wherein reduction of the test amount of specific activation relative to the first
amount of specific activation indicates that the candidate pharmacological agent is a lead
compound for a pharmacological agent which disrupts the GTPase activation activity of PARG,
30 and wherein increase of the test amount of specific activation relative to the first amount of
specific activation indicates that the candidate pharmacological agent is a lead compound for a
pharmacological agent which enhances the GTPase activation activity of PARG.

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51. The method of claim 50, wherein the GTPase specifically activatable by the PARG GTPase activating domain is Rho.

52. A method for identifying lead compounds for a pharmacological agent useful in the
5 diagnosis or treatment of disease associated with PARG binding to a protein containing a PDZ4 domain, comprising

forming a mixture comprising a PARG polypeptide or unique fragment thereof containing a PDZ4 domain binding site, a protein containing a PDZ4 domain which selectively binds the PARG PDZ4 domain binding site, and a candidate pharmacological agent,

10 incubating the mixture under conditions which, in the absence of the candidate pharmacological agent, permit a first amount of selective binding of the protein containing a PDZ4 domain by the PDZ4 domain binding site, and

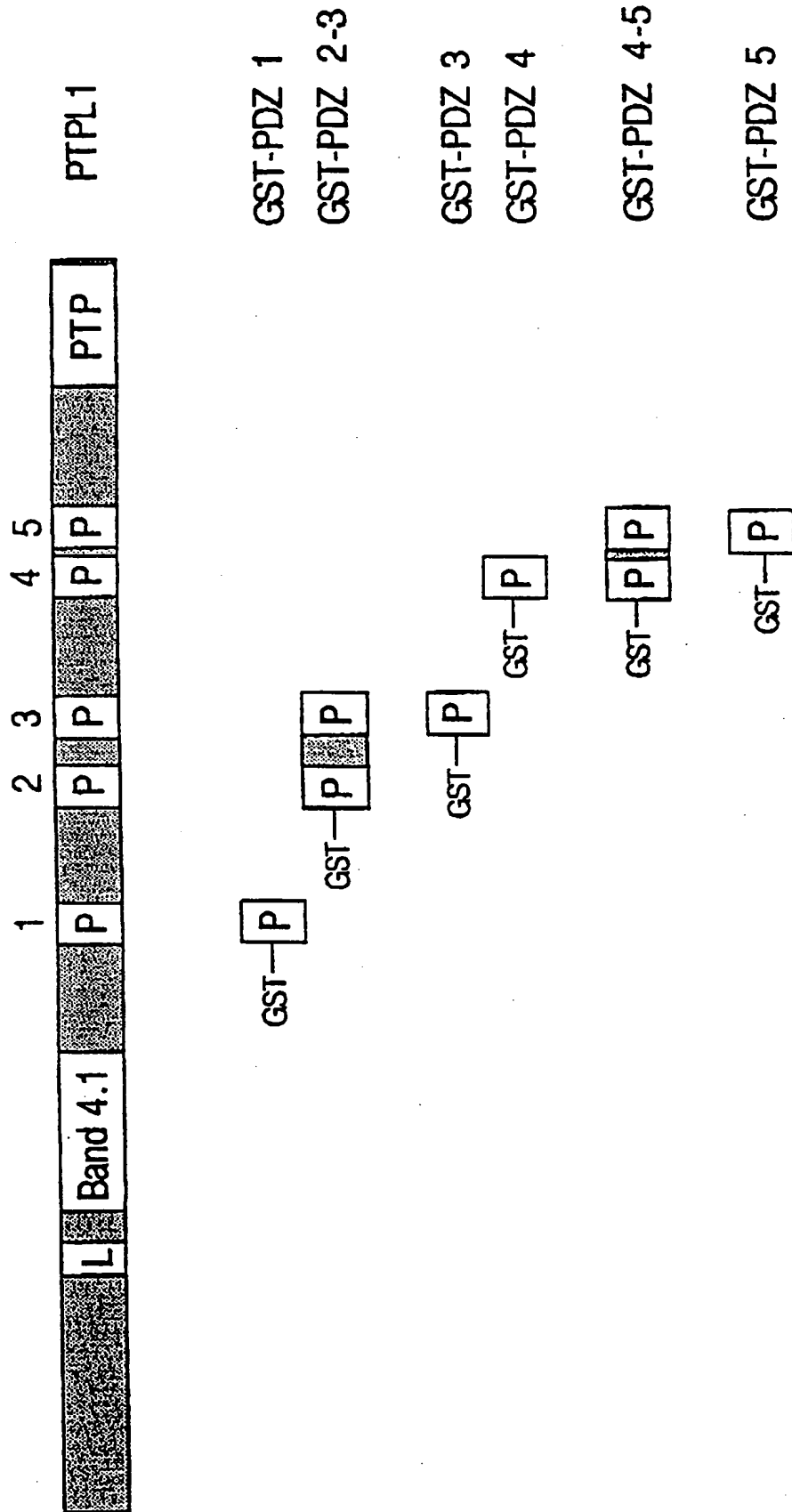
detecting a test amount of selective binding of the protein containing a PDZ4 domain by the PDZ4 domain binding site, wherein reduction of the test amount of selective binding relative
15 to the first amount of selective binding indicates that the candidate pharmacological agent is a lead compound for a pharmacological agent which disrupts selective binding of a protein containing a PDZ4 domain by a PARG polypeptide containing a PDZ4 domain binding site and wherein increase of the test amount of selective binding relative to the first amount of selective binding indicates that the candidate pharmacological agent is a lead compound for a
20 pharmacological agent which enhances selective binding of a protein containing a PDZ4 domain by a PARG polypeptide containing a PDZ4 domain binding site.

53. The method of claim 52 wherein the protein containing a PDZ4 domain is PTPL1.

25

Fig. 1

A



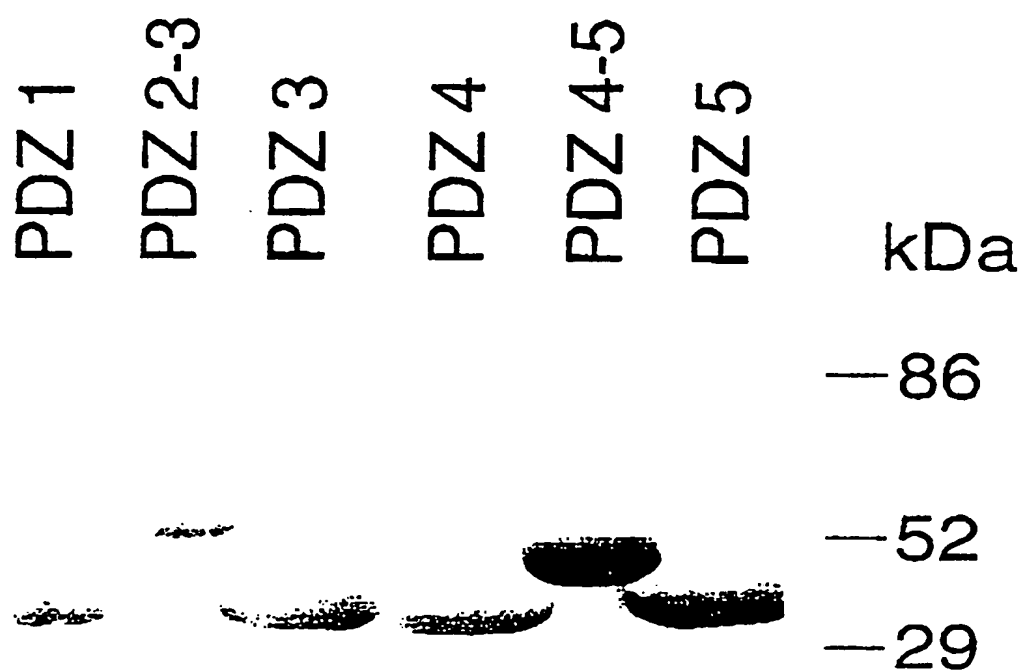
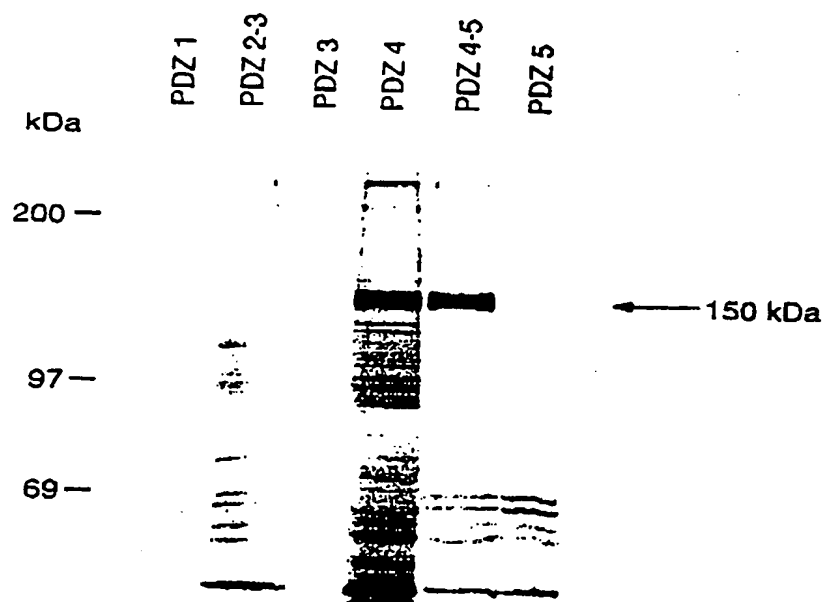
*Fig. 1***B**

Fig. 2

A**Fig. 3**

MTAHKOKKTKKKRAWASGOLSTDITTSSEHGLKSLSSNSIFOPDYIKELVNDIRKFSHILLYLKEAIFSDCFKEVIHIRLE 80
ELLRLVLSIMNKHONLNSVDLQNAEMLTAKVKAVNFTEVNEENKNOLFOEVFSSIETLAFTFGNILTNFLMGDVGNDSF 160
LRLPVSRETKSFENVSVESVDSSSEKGNFSPLELDNVLLKNTDSIELALSYAKTWSKYTKNIYSWVEKXLNLELESTRNM 240
VKLAEATRITNIGIOEFMPLOSLFTNALLNDIESSHLOOTIAALOANKFVQPLLGRKNEMEKORKEIKELWKOEONKMLE 320
AENALKKAKLLCMORODEYEKAKSSMFR~~AEFEHLSS~~GGGLAKNLNKOLEKKRRLEEEALOKVEEADELYKVCVTNVEERR 400
NDVENTKREILAQLRTL VFODLT LKAVTVNLFHMOHLOAASLADRLOSLCGSAKLYDPGGQYSEFVKATNSTEEKVDG 480
NVNKHNLSSQPSGFGPANSLEDVVRLPDSSNKIEEDRCSNSADITGPSFIRSWTFGMFSDSESTGGSSSESRLDSESISP 560
GDFHRKLPRTPSSGTMSSADDLDEREPPSPSETGPNLSLGTFFKTLMSKAALTHKFRKLRSPKCRDCEGIVVFOGVECEE 640
CLLVCHRKCLENLVIICGHOKLPGKIHLEGAFFTLVAKKEPDGIPFILKICASEIENRALCLOGIYRYCGNKIKTEKLCL 720
ALENGMHLVDISEFSSHDICDVLKLYLROLPEPFI LFRLYKEFIDLAKETOHVNEEQETKKSLEDKKWPNMCIEINRIL 800
LKSKDLLROLPASNFNSLHFLIVHLKRVVDHAEENKMNSKNLGVIFGPSLIRPRPOTAPITISSLAEYSNOARLVEFLIT 880
YSOKIFDGSLOPODVMCSIGVVDQGCFFPKLLSPPEERDIERSHMSLFFSSKEDIHTSESESKIFERATSFEESERKQNAL 960
GKCDACLSOKAOLLLDQEAESASQKIEDGKAPKPLSLKSDRSTNNVERHTPRTKIRPYSLPVDRLLLASPPNERNGRNMG 1040
NVNLDKFCKNPAFEGVNRKDAATTVCSEKNGFDQOOTLOKIDOKOYEONSLTAKYTHIMP3ALQEKGYTTSLOISGDHSIN 1120
ATOPSKPYAEPVRSVREASERRSSDSYPLAPVRAPRTLQPOHWTTFYKPHAPIISIRGNEEKPASPSAACPPGTDHDPHG 1200
LVVKSMPDPDKASACPGOATGPKEDSEELGLPDVNPQCORPRLKRMQOFEDLEDEIPOQFV 1261

*Fig. 3***B**

E L D N V L L K N T D S I E L A L S Y A K T W S K Y T K N I V S W V E K K L N L PARG
 F I D K L L I S R T D G V D V A F E R T K A W S T Y S K D V I S Y V R A R I Q L ZK669. 1a
 E L E S T R N M V K L A E A T R T N T G I O E F H P L Q S L F T N A L L N O I E PARG
 E O D H A R K V H T L V D T S R R D I N - K P F H P L R E T F E N S F D T E V E ZK669. 1a
 S S H L L O O T I A A L Q A N K F V O P L L G R K N E M E K O R K E I K E L W K PARG
 H V T H T K E T T E H L K - D R V V E A L D A R R K E H D T V R N A L K V E W T ZK669. 1a
 - - - - - - - - - - Q E O N K M L E A E N A L K K A K L L C M O R O D E PARG
 K A T K S L H D C E E S Y E K S K I T L R M R E E A L K K A R E S C L R T E S - ZK669. 1a
 Y E K A K S S M F R A E E E H L S S S G G L A K N L N K O L E K K R R L E E E A PARG
 - - - - - - - - - - S P P E R E A S R R R R R D L E K K S R A V E E A ZK669. 1a
 L Q K V E E A D E L Y K V C V T N V E E R R N D V E N T K R E I L A O L R T L V PARG
 H I K K E E A E R Q V V S I T A E L R K K R R D I D K T K E S V V E R L R E L I ZK669. 1a
 F Q C D L T L K A V T V N L F H M O H L O A A S L A D R L O S L C G S A K L Y D PARG
 F Q C E O T T K A C T V H Y F T S L A A L W A R L P G A F H E L S N A T R D Y Q ZK669. 1a
 P G Q E Y S E F V - - - - K A T N S T E E E K V D G N V N K H L N S S O - P S PARG
 P G T E Y M A F L D T L P T R A A S S S S L V R S D R S I D E G V A S C D G S S ZK669. 1a
 G F G P - - - - A N S L E D V V R L P D S PARG
 S L T S L R R N A I N P D D E G A L P D T ZK669. 1a

C

Fig. 3

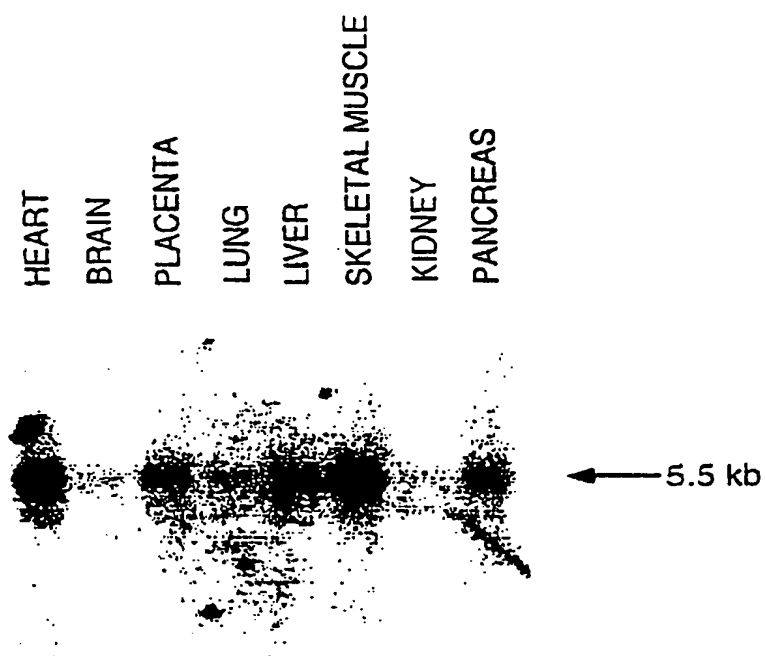


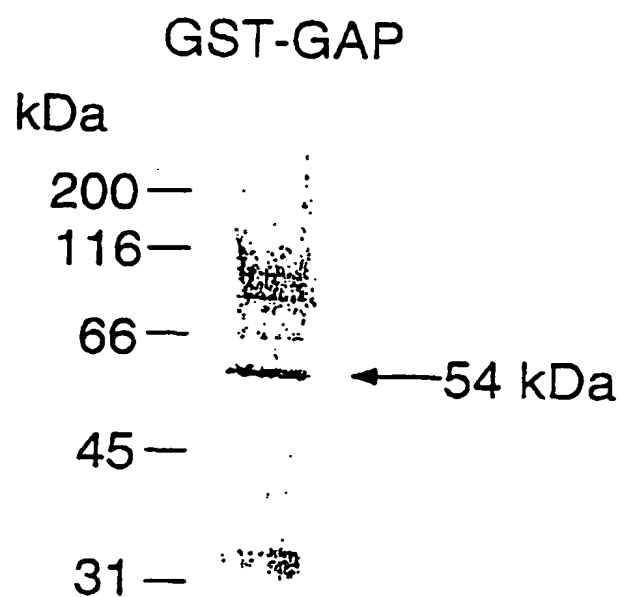
PARG



ZK669.1a

Fig. 4



*Fig. 5***A**

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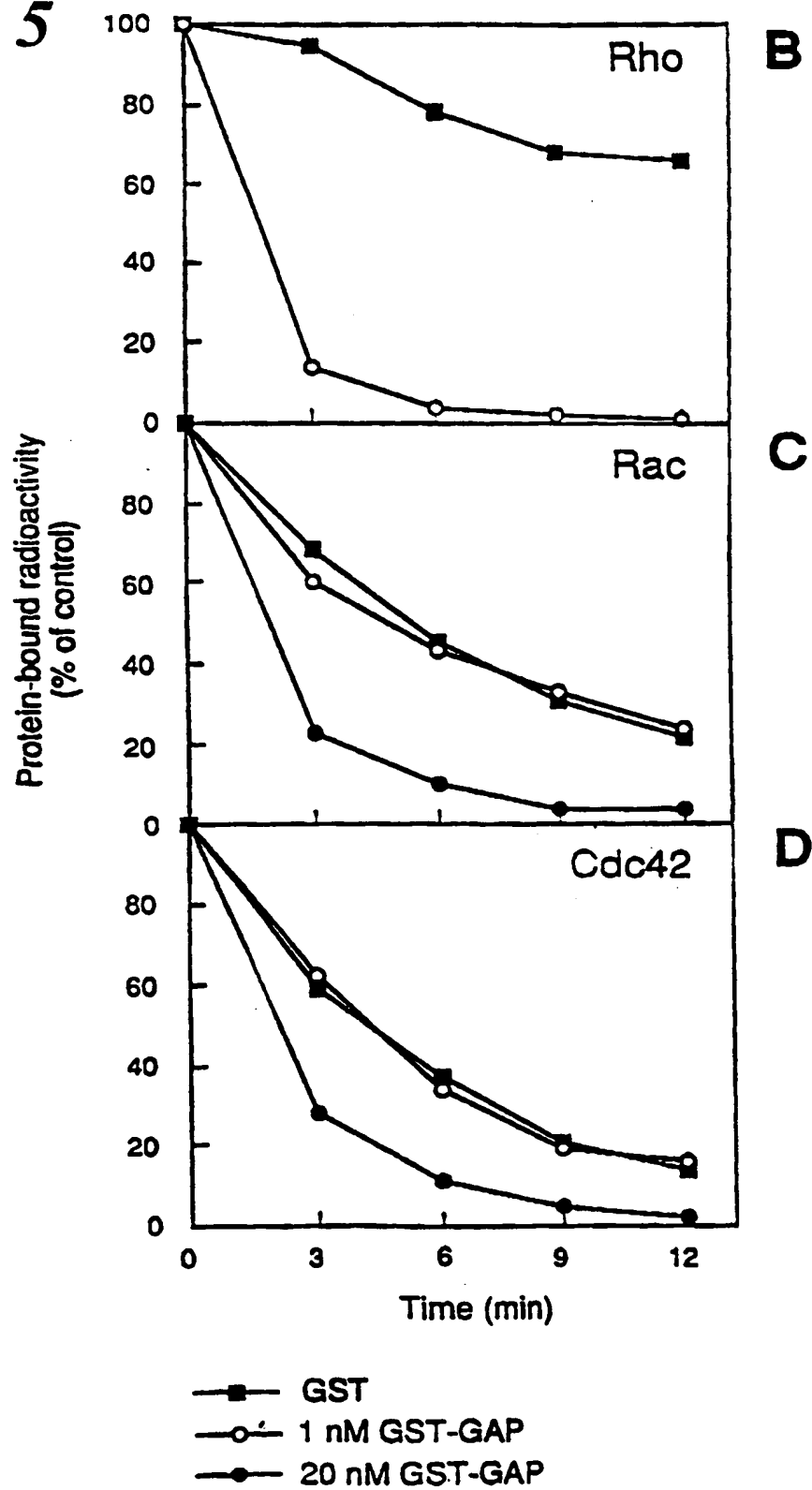
Fig. 5

Fig. 6



INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 98/03323

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C07K14/47 C12N1/21 C12N5/10 C12N9/16
A61K38/17 A61K39/395 A61K38/46 A61K31/70 G01N33/68
C12Q1/44 C12Q1/42

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K A61K G01N C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category ° | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|--|-----------------------------------|
| X | SARAS J. AND HELDIN C.-H.: "PDZ domains bind carboxy-terminal sequences of target proteins"
TIBS TRENDS IN BIOCHEMICAL SCIENCES, vol. 21, no. 12, December 1996, pages 455-458, XP004063028 | 5-7,
13-30,
38-40,
44-46 |
| Y | see page 455; table 1 | 31-33,
41-43,
50-53 |
| A | see page 456; figure 1H

see page 457, middle column - left-hand column

-/-- | 34-37,
47-49 |

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

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"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

13 July 1998

Date of mailing of the international search report

28.07.98

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Authorized officer

Macchia, G

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/03323

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
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Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: although claims 31-42, as far as in vivo methods are concerned, and 43, 47-49 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

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